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OM protein - protein search, using sw model

Run on: April 6, 2004, 14:10:29 ; Search time 23 Seconds
(without alignments)
-733.987 Million cell updates/sec

Title: US-09-787-844-2

Perfect score: 1792
Sequence: 1 KRQRQAAGEMGARGAL.....PSWPLLPFLNALPLGPV 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/5A-COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/5B-COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PTCUS-COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	96.4	314	3 US-09-008-271A-3	Sequence 3, Appli
2	1728	96.4	314	4 US-09-907-794A-257	Sequence 257, App
3	1728	96.4	314	4 US-09-905-125A-257	Sequence 257, App
4	1728	96.4	314	4 US-09-902-775A-257	Sequence 257, App
5	1723	96.1	314	4 US-09-023-942A-6	Sequence 6, Appli
6	1701	94.9	312	4 US-09-023-942A-4	Sequence 4, Appli
7	1419	79.2	306	4 US-09-386-642-53	Sequence 53, Appli
8	1108.5	61.9	285	4 US-09-023-942A-26	Sequence 26, Appli
9	574	32.0	290	4 US-09-386-653A-7	Sequence 7, Appli
10	554	30.9	299	3 US-08-944-483-66	Sequence 66, Appli
11	550	30.7	315	4 US-09-386-653A-9	Sequence 9, Appli
12	541.5	30.2	328	4 US-09-386-642-11	Sequence 11, Appli
13	540.5	30.2	319	4 US-09-386-642-12	Sequence 12, Appli
14	531.5	29.7	317	4 US-09-386-629-7	Sequence 7, Appli
15	531.5	29.7	317	4 US-09-907-794A-263	Sequence 263, App
16	531.5	29.7	317	4 US-09-905-125A-263	Sequence 263, App
17	531.5	29.7	317	4 US-09-902-775A-263	Sequence 263, App
18	528.5	29.5	270	2 US-08-978-404B-8	Sequence 8, Appli
19	515	28.7	273	2 US-09-016-366A-19	Sequence 19, Appli
20	515	28.7	273	2 US-08-978-404B-14	Sequence 14, Appli
21	514	28.7	274	2 US-09-016-366A-21	Sequence 21, Appli
22	514	28.7	274	2 US-08-978-404B-16	Sequence 16, Appli
23	512	28.6	267	2 US-09-016-366A-23	Sequence 23, Appli
24	512	28.6	267	2 US-08-978-404B-18	Sequence 18, Appli
25	512	28.6	276	2 US-09-016-366A-15	Sequence 15, Appli
26	512	28.6	276	2 US-08-978-404B-21	Sequence 21, Appli
27	511	28.5	638	2 US-08-681-151-3	Sequence 3, Appli

Sequence 6, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 63, Appli
Sequence 17, Appli
Sequence 12, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 69, Appli
Sequence 25, Appli

ALIGNMENTS

RESULT 1
US-09-008-271A-3
; Sequence 3, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT03
; CLONE: 789927
; SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
US-09-008-271A-3

Query Match 96.4%; Score 1728; DB 3; Length 314;
Best Local Similarity 100.0%; Pred. No. 6.9e-166;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAELGRWPWGSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAELGRWPWGSLR 60

QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSPSPFWSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSPSPFWSLQAYYTRYF 120

QY 134 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGMYIK 193
DB 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGMYIK 180

QY 194 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLMYQIGVSWGVCGRPNRPVYTKHIFWIOKLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLMYQIGVSWGVCGRPNRPVYTKHIFWIOKLMAQSGMSQDPSPWPLL 300

QY 314 FFPLLWALPLLPV 327
DB 301 FFPLLWALPLLPV 314

RESULT 2

US-09-907-794A-257
Sequence 257, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794A-257

Query Match

Best Local Similarity 96.4%; Score 1728; DB 4; Length 314;

Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAELGRWPWGSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAELGRWPWGSLR 60

QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSPSPFWSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSPSPFWSLQAYYTRYF 120

QY 134 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGMYIK 193
DB 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGMYIK 180

QY 194 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSFHTLQEVQVAIINNSMNCNHLFLKYSFRKDIFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLMYQIGVSWGVCGRPNRPVYTKHIFWIOKLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLMYQIGVSWGVCGRPNRPVYTKHIFWIOKLMAQSGMSQDPSPWPLL 300

QY 314 FFPLLWALPLLPV 327
DB 301 FFPLLWALPLLPV 314

RESULT 3

US-09-905-125A-257
Sequence 257, Application US/09905125A

Patent No. 6664376

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905/125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-125A-257
Query Match 96.4%; Score 1728; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 6.9e-166;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPSQEAAPLSGCGRRVITSRIVGGEDALGRWPNQGSRLR 73
DB 1 MGARGALLALLARAGLRKPSQEAAPLSGCGRRVITSRIVGGEDALGRWPNQGSRLR 60
QY 74 LWDSHVCGVSLLSHRWALTAACFETYSLSLSDPSGVMVQFGLTSMPSFMSLOAYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACFETYSLSLSDPSGVMVQFGLTSMPSFMSLOAYTRYF 120
QY 134 VSNIIYSPRYLGNSPYDIALVLSAPVYTKHTQICLOASTFEFENRTDCWVTGWGIK 193
DB 121 VSNIIYSPRYLGNSPYDIALVLSAPVYTKHTQICLOASTFEFENRTDCWVTGWGIK 180
QY 194 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWIKLMAQSGNSQDPSWPLL 313
DB 241 PLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWIKLMAQSGNSQDPSWPLL 300
QY 314 FFPLLWALPLLGPV 327
DB 301 FFPLLWALPLLGPV 314
RESULT 4
US-09-902-775A-257
Sequence 257, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-775A-257

Query Match 96.4%; Score 1728; DB 4; Length 314;
Best Local Similarity 100.0%; Pred. No. 6.9e-166;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPGQSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPGQSLR 60
QY 74 LWDHVGCVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPFWSLQAYTRYF 133
DB 61 LWDHVGCVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPFWSLQAYTRYF 120
QY 134 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 193
DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
QY 194 EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGCGRRPNRPVYTNISHFHWIQLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLWYQIGVSWGCGRRPNRPVYTNISHFHWIQLMAQSGMSQDPSPWPLL 300
QY 314 FFLLWALPLLGPV 327
DB 301 FFLLWALPLLGPV 314

RESULT 5
US-09-023-942A-6
; Sequence 6, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023, 942A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P05101/97
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P04022/97
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-942A-6

Query Match 96.1%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 2.2e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPGQSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPGQSLR 60
QY 74 LWDHVGCVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPFWSLQAYTRYF 133
DB 61 LWDHVGCVSLLSHRWALTAHCFETYSDLSDPGMMVQFGQLTSPFWSLQAYTRYF 120
QY 134 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 193
DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
QY 194 EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSPHTLQEVQVVAIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGCGRRPNRPVYTNISHFHWIQLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLWYQIGVSWGCGRRPNRPVYTNISHFHWIQLMAQSGMSQDPSPWPLL 300
QY 314 FFLLWALPLLGPV 327
DB 301 FFLLWALPLLGPV 314

RESULT 6
US-09-023-942A-4
; Sequence 4, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: POS101/97
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: PFO422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-942A-4

Query Match 94.9%; Score 1701; DB 4; Length 312;
Best Local Similarity 99.0%; Pred. No. 3.6e-163;
Matches 311; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 14 MGAGALLALLIALLARGLKPSQAAPLSGPCGRRVITSIRIVGGEDAEELGRWPQGSRLR 73
DB 1 MGAGALLALLIALLARGLKPSQAAPLSGPCGRRVITSIRIVGGEDAEELGRWPQGSRLR 60
QY 74 LWDSHVCGVSLLSHRWALTAACHFETYSDLSPSGMWVQFGOLTSMPFWSLQAYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACHFET--DLSDPSGMVQFGOLTSMPFWSLQAYTRYF 118
QY 134 VSNYLSRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 193
DB 119 VSNYLSRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 178
QY 194 EDEALPSHTLQEVQVAIINNSMCHLFLKYSFRKDIQDMVCAGNAQGGKACFGDSGG 253
DB 179 EDEALPSHTLQEVQVAIINNSMCHLFLKYSFRKDIQDMVCAGNAQGGKACFGDSGG 238
QY 254 PLACNKNGLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSWPLL 313
DB 239 PLACNKGDLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSWPLL 298
QY 314 FPELLWALPLGPV 327
DB 299 FPELLWALPLGPV 312

RESULT 7
US-09-386-642-53
Sequence 53, Application US/093866642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Cordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028

CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 53
LENGTH: 306
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
OTHER INFORMATION: human protease P in CFEK2 zymogen vector
US-09-386-642-53

Query Match 79.2%; Score 1419; DB 4; Length 306;
Best Local Similarity 89.7%; Pred. No. 9e-135;
Matches 261; Conservative 4; Mismatches 20; Indels 6; Gaps 2;
QY 23 ALLARAGLRKP---ESQEAAPLSGCGRRVITSIRIVGGEDAEELGRWPQGSRLRWDHSV 79
DB 11 ALLGTTFGCGVPDYKDDDAALAAAFDD---DDKIVGGYALELGRWPQGSRLRWDHSV 67
QY 80 CGVSLLSHRWALTAACHFETYSDLSPSGMWVQFGOLTSMPFWSLQAYTRYFVSNYIL 139
DB 68 CGVSLLSHRWALTAACHFETYSDLSPSGMWVQFGOLTSMPFWSLQAYTRYFVSNYIL 127
QY 140 SPRLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIKEDALP 199
DB 128 SPRLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIKEDALP 187
QY 200 SPHTLQEVQVAIINNSMCHLFLKYSFRKDIQDMVCAGNAQGGKACFGDSGGPLACNK 259
DB 188 SPHTLQEVQVAIINNSMCHLFLKYSFRKDIQDMVCAGNAQGGKACFGDSGGPLACNK 247
QY 260 NGLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPDSW 310
DB 248 NGLWYQIGVVGWVGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPDSW 298

RESULT 8
US-09-023-942A-26
Sequence 26, Application US/09023942A
Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: POS101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PFO422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S

```
/
/
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 11168
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742 4343
/ TELEFAX: (516) 742 4366
/ TELEX: 230 501 SANS UR
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 285 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-023-942A-26

Query Match 61.9%; Score 1108.5; DB 4; Length 285;
Best Local Similarity 68.8%; Pred. No. 1.6e-103;
Matches 196; Conservative 36; Mismatches 50; Indels 3; Gaps 2;

QY 42 LSGPCGRVLTSRVGGEDAEELGRWPGQSLRWDSHVCGVSLSHRWALTAHCFETYS 101
DB 3 LSGPCGHRITPSRVGGDDAEELGRWPGQSLRWGNHLCATILNRRWLTAAHCFQ--K 60
QY 102 DLSPPGMMVQFGLTSMPSFSLQAYTRYFYVSNTYLSPRYLGNSPYDIALVKLSAPVT 161
DB 61 D-NDPFDWTQFGLTSRPSLWNLQAYSNRYQIEDIFLSPKYSEQYENDIALLLKSSPVT 119
QY 162 YTXHIQICQASTFPEKRTDCWVTGWYIKEDALPSHTLOEYQVAIINNSMCHLF 221
DB 120 YNFIQICLNLSTYKFNRTDCWVTGWGAGDESLPNTLQEVQVAIINNSMCHMY 179
QY 222 LKYSFRKDIQDMVCAGNAQGGKDACFGDSGGLACNKGMLTYQIGWSGVGCGRPNRP 281
DB 180 KXPDRFRTNGDMVCAGTPSGGKDACFGDSGGLACQDQTVWYQVGVWSGIGCGRPNRP 239
QY 282 GVTNISHHFEWTKLMAQSGMQPDPSPWLLFFPLNLWALPLGP 326
DB 240 GVTNISHYNIQSTMIENGLLRDPVPLLLFLTLAWASSLLRP 284

RESULT 9
US-09-386-653A-7
/ Sequence 7, Application US/09386653A
/ Patent No. 6458564
/ GENERAL INFORMATION:
/ APPLICANT: Andrade-Gordon, Patricia
/ APPLICANT: Darrow, Andrew
/ APPLICANT: Qi, Jian-shen
/ TITLE OF INVENTION: DNA encoding the novel human serine
/ TITLE OF INVENTION: protease I
/ FILE REFERENCE: ORT-1032
/ CURRENT APPLICATION NUMBER: US/09/386,653A
/ CURRENT FILING DATE: 1999-08-31
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 290
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-386-653A-7

Query Match 32.0%; Score 574; DB 4; Length 290;
Best Local Similarity 42.6%; Pred. No. 1.1e-49;
Matches 123; Conservative 44; Mismatches 100; Indels 22; Gaps 8;

QY 17 RGALLLALLRAGLRKPESQEAAPLSGPCGRRVITSRIYVGGDAELGRWPGQSLRLMD 76
DB 3 RPAAPVPLLLLLCFGSQAKAATA-----CGRPMLNRMVGGQDTQEGEWFGVSIQRNG 56
QY 77 SHVCGVSLSHRWALTAHCFETYSDLSDPSGMMVQFG--QLTSMPSFSLQAYTRYFYV 134
DB 57 SHFCGGSLLAQWVLTAAHCFER---NTSETSLVQVLLGARQLVQP-----GPHMYAR--V 107
QY 135 SNLYSPRYLGN--SPYDIALVKLSAPVTRYTKHIQICQASTFPEKRTDCWVTGWYIK 193

DB 108 QRVESNPLYQGTASSADVALVEAPVPFTNYILPVCLPDPSPVIFETGMNCWVTGWSPPS 167
QY 194 EDEALPSPHTLQEVQVAIINNSMCHLFK---YSFR-KDIFGDMVCAGNAQGGKDACFG 249
DB 168 EEDLLPEPRILQKLAVPIITPKCNLLYSKDTFEGYQPKTKNDMLCAGFECKGKDACG 227
QY 250 DSGGPLACNKGMLTYQIGVWSGVGCGRPNRPQVYTNISHHFEWIKLM 298
DB 228 DSGGPLVCLVQSWLQAGVISWEGCARQNRPGVYIRVTAHHWIIIRII 276

RESULT 10
US-08-944-483-66
/ Sequence 66, Application US/08944483
/ Patent No. 6232456
/ GENERAL INFORMATION:
/ APPLICANT: COHEN, MAURICE
/ APPLICANT: COLPITTS, TRACEY L.
/ APPLICANT: FRIEDMAN, PAULA N.
/ APPLICANT: GRANADOS, EDWARD N.
/ APPLICANT: KLUSS, MICHAEL R.
/ APPLICANT: RUSSELL, JOHN C.
/ APPLICANT: STEWART, KENT D.
/ APPLICANT: STROUPE, STEVEN D.
/ TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
/ TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
/ TITLE OF INVENTION: OF THE PROSTATE
/ NUMBER OF SEQUENCES: 76
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Abbott Laboratories
/ STREET: 100 Abbott Park Road
/ CITY: Abbott Park
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: Fast-SEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA: US/08/944,483
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Becker, Cheryl L.
/ REGISTRATION NUMBER: 35,441
/ REFERENCE/DOCKET NUMBER: 6183 US.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 847/935-1729
/ TELEFAX: 847/938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 66:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 299 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: No. 62324566
/ US-08-944-483-66

Query Match 30.9%; Score 554; DB 3; Length 299;
Best Local Similarity 41.2%; Pred. No. 1.2e-47;
Matches 127; Conservative 41; Mismatches 90; Indels 50; Gaps 9;

QY 55 IVGGDAELGRWPGQSLRWDSHVCGVSLSHRWALTAHCFETYSDLSDPS-----GW 109
DB 1 ITGSSAVAGQNPWQVSIYEGVHVGGSLSVEQWVLSAAHCF-----PSEHKEYA 52
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QY 110 MYQFG--QLTSMPSFWSLQAYVYTRFVSVNIYLSPRYL--GNSPYDIALVKLSAPVYTKHI 166
Db 53 EVKGAHQDLS-----YSDAKVST--LKDIIHPSPYLOEGSGQDIALQLSRPITFSRYI 106
QY 167 QPICQASTFEFENRTDCWVTGWGXYKEDALPSPHTLQEVQVAIINNSMCNHLF---LK 223
Db 107 RPICLPAANASFPNGLHCTVTCGWGHVAPSVLLTPKPLQQLLEVPLISRETCLNIDAK 166
QY 224 YSFRKDIQDMVCAGNAQGGKDACFGDSGGPLACNKNGLWYQIGVSVGWCGGRNRPV 283
Db 167 PEEPHFVQEDMVCAGYVSGGKDACQDSGGPLSCPEVGLWYLTGIVSGWDGACGARNRPV 226
QY 284 YNNISHHFEWIO-----KLMAQSGMSQDDPSW-----PLFFPPLL 318
Db 227 YTLASSYASWIGSKYTELQPRVVPQTQESQDNLCSGSHLAFSSAPAGQLLRPIFLPLG 286
QY 319 WALPLLGP 326
Db 287 LALGLLSP 294

RESULT 11
US-09-386-653A-9
; Sequence 9, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Darrow, Andrew
; TITLE OF INVENTION: DNA encoding the novel human serine
; TITLE OF INVENTION: protease T
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
; OTHER INFORMATION: Of Protease T in a zymogen activation construct
US-09-386-653A-9
Query Match 30.7%; Score 550; DB 4; Length 315;
Best Local Similarity 40.3%; Pred. No. 3.3e-47;
Matches 123; Conservative 46; Mismatches 104; Indels 32; Gaps 10;

QY 14 MGARGA-----LLALLLAR-----AGLRKPESQEAAPLSGPCGRVITSRIYGGED 60
Db 1 MDSKSSQKSRLLLLVSNLLCGQVSDYKDDDDVDAALAAPFDD---DDKIVGGYA 57
QY 61 AELGRWPQGSRLWDSHVCVGLSLSHRWALTAHCFETYSDLSDPSCMVMQFG--QLTS 118
Db 58 LEEGEWPQVSIQRNGSHPCGSGSLIAEQWLVLTAAHCFR---NTSETSLYQLLQARQLVQ 114
QY 119 MFSFWSLQAYVYTRFVSVNIYLSPRYLN--SPYDIALVKLSAPVYTKHIQICLQASTFE 177
Db 115 P-----GPHAWYAR--VRQVESNPLYCGTASSADVALVEAFVPTNYILVCLPDPDSVI 168
QY 178 FENRTDCWVTGWGXYKEDALPSPHTLQEVQVAIINNSMCNHLFLK---YSFR-KDIPGD 233
Db 169 PETGMNCWVTGWGSPSEEDLLPEPRILQKLAVIDTPKCNLLYSKDTFPGYQPKTIKD 228
QY 234 MYCAGNAQGGKDACFGDSGGPLACNKNGLWYQIGVSVGWCGGRNRPVYTNISHHFEW 293
Db 229 MLCAGFEQKDKACKDGGPLVCLVGSWLGQVSVISWEGCARGNQREGVIRVTAHHNW 288
QY 294 IQKLM 298
Db 289 IHRII 293
```

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RESULT 12
US-09-386-642-11
; Sequence 11, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Gene
; OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11
Query Match 30.2%; Score 541.5; DB 4; Length 328;
Best Local Similarity 39.3%; Pred. No. 2.5e-46;
Matches 128; Conservative 51; Mismatches 98; Indels 49; Gaps 11;

QY 14 MGARGA-----LLALLLAR-----AGLRKPESQEAAPLSGPCGRVITSRIYGGED 60
Db 1 MDSKSSQKSRLLLLVSNLLCGQVSDYKDDDDVDAALAAPFDD---DDKIVGGYA 57
QY 61 AELGRWPQGSRLWDSHVCVGLSLSHRWALTAHCFETYSDLSDPSCMVMQFG--114
Db 58 LEAGQWPQVSIYEGVHVHVCGLSVSEQWVLSAAHCF-----PSEHKEAYEVKLG 109
QY 115 -QLTSMPSFWSLQAYVYTRFVSVNIYLSPRYL--GNSPYDIALVKLSAPVYTKHIQICLQ 172
Db 110 HQDLS-----YSDAKVST--LKDIIHPSPYLOEGSGQDIALQLSRPITFSRIICLP 163
QY 173 ASFFEFENRTDCWVTGWGXYKEDALPSPHTLQEVQVAIINNSMCNHLF---LKYSFRKD 229
Db 164 AANASFPNGLHCTVTCGWGHVAPSVLLTPKPLQQLLEVPLISRETCLNIDAKPEPHF 223
QY 230 IFQDMVCAGNAQGGKDACFGDSGGPLACNKNGLWYQIGVSVGWCGGRNRPVYTNISH 289
Db 224 VQEDMVCAGYVEGKDKACQDSGGPLSCPEVGLWYLTGIVSGWDGACGARNRPVYTLASS 283
QY 290 HFEWIO-----KLMAQSGMSQPD 307
Db 284 YASWIOSKYTELQPRVVPQTQESQPD 309
```

```
RESULT 13
US-09-386-642-12
; Sequence 12, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
```

OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-12

Query Match 30.2%; Score 540.5; DB 4; Length 319;
Best Local Similarity 41.4%; Pred. No. 3.1e-46;
Matches 127; Conservative 43; Mismatches 98; Indels 39; Gaps 10;

QY 23 ALLARAGLRKP---ESQEAAPLSGCGRRVITSRIVGGEDAEIGRWPMQGSRLWDSDV 79
DB 11 ALLTTTGGVDPYKDDDDAALAPDD---DDKIVGGYALEAGOWPMQVSVITYGVHV 67
QY 80 CGVSLSHRWALTAHCFETYSDLSDFS-----GMVQFG--QLTSMPSFWSLQAYTRY 132
DB 68 CGGSLVSEQWLSAAHCF-----PSEHKAEAYEVLGAHQIDS-----YSEDAKVST- 114
QY 133 FVSNILSPRYL-CNSPYDIALVKLSAPVYTKHIQICICLOASTFFEFENRTDCWVTGWY 191
DB 115 -LKDIILHPSYLOEGSGDIALQLSRITFSYIRIDICLPANASFPFNGLHCTVTGWGH 173
QY 192 IKEDEALSPHTLQEVQVAIINNSMCHLF---LKYSFRKIDFGDMVCAGNAGGKDACF 248
DB 174 VAPSVLLTPKPLQQLVPLISRETCLNYIDAKPEPHFVQEDMVCAGYVGGKDAQ 233
QY 249 GDSGGLACNKNGLWYQIGVSWGCGRRPGRVYTNISHHFEWIO-----KLMAQ 300
DB 234 GDSGGLSCFVBEGLWYLTGIVSMGDACGARNRPGVYTLASSYASWISQKVTQLQPRVFP 293
QY 301 SGMSQPD 307
DB 294 TQESQPD 300

RESULT 14

US-09-386-629-7

Sequence 7, Application US/09386629

Patent No. 6426199

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew L.

APPLICANT: Qi, Jensen

APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Identification and Characterization of the complementary

FILE REFERENCE: ORT-1030

CURRENT APPLICATION NUMBER: US/09/386,629

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 7

LENGTH: 317

TYPE: PRT

ORGANISM: Homo sapiens

US-09-386-629-7

Query Match 29.7%; Score 531.5; DB 4; Length 317;
Best Local Similarity 36.0%; Pred. No. 2.5e-45;
Matches 111; Conservative 57; Mismatches 115; Indels 25; Gaps 6;

QY 15 GARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEIGRWPMQGSRL 74
DB 13 GCLGTFSLLLATAIL---NAARIPVACRPQOLNVRVGGEDSTSEWPMVISIQ 69
QY 75 WDSHVCVGLLSHRAWLTAHCFETYSDLSDPGVMYVQGLTSMPSFWSLQAYTRY-YF 133
DB 70 NGTHCAGSLTSRWVITAAHCFK--DNLNKPVLFSVLLGA-----WQLGNPGRSQK 120
QY 134 VSNILSPR-----VLGNSPYDIALVKLSAPVYTKHIQICLOASTFFEFENRTDCWVTGW 189
DB 121 VGVAVVEPHVYVSKKACADIALVRLRSIQSERVLPICLPDASHLPFPPNTHCWISGW 180
QY 190 GYIKEDALSPHTLQEVQVAIINNSMCHLFKYSFRKIDFGDMVCAGNAGGKDACFG 249
DB 181 GSIQDGVLPHPQLQLKVPIDSEVCSHLYWRGACQGPITEDMLCAGVLEGERDACLG 240

QY 250 DSGGFLACNKNGLWYQIGVSWGCGRRPGRVYTNISHHFEWIOKLM-----AQS 301
DB 241 DSGGFLACQVDGAWLLAGIISWEGGCAERNRPGVYISLSAHSRWVKIVQGVQLRGAQG 300
QY 302 GMSQPDPS 309
DB 301 GGLRAPPS 308

RESULT 15

US-09-907-794A-263

Sequence 263, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Christoppher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911


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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 263
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-263

Query Match      29.7%; Score 531.5; DB 4; Length 317;
Best Local Similarity 36.0%; Pred. No. 2.5e-45;
Matches 111; Conservative 57; Mismatches 115; Indels 25; Gaps 6;

QY 15 GARGALLLALLARAGLRKPESQEAAPLSGPGCRRVITTSIVGGEDAELGRNFWQGSLEL 74
Db 13 GCLGTFSTLLLLASTAL---NAARIPVPACGKPGQLNRVVGEDSTDSWFWIVSIQK 69

QY 75 WDSHVCGVSLSHRWALTAACHFETYSDDLSDPSGWMVQFQQLTSMFSWLSQAYYTR-YF 133
Db 70 NGTHHCAGSLTTSRWVITAAHCFK--DNLNKPILFVLLGA-----WOLGNPGRSQK 120

QY 134 VSNITLSPR---YLGNSPYDIALVLSAPVYTKHIQICLOASTFEFENRTDCWVTGW 189
Db 121 VGVAVVEPHYPYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGW 180

QY 190 GYIKEDALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDI FGDVMVCAGNAQGGKDACFG 249
Db 181 GSIQDGVLPHPQTLQKLVPIIDSEVCVSHLYWRGAGQGPITEDMLCAGYLEGERDACL 240

QY 250 DSGGPLACNKNGLWYQIGVSWGVGCGRPNRPGVYTNISHHFEWIOKLM-----AQS 301
Db 241 DSGGPLMCQVDGAWLLAGIISWEGECAERNRPGVITSLAHSRWSWEKIVGVQVLRG 300

QY 302 GMSQPDPS 309
Db 301 GGALRAPS 308
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Search completed: April 6, 2004, 14:14:13
Job time : 24 secs

GenCore version 5.1.1.6
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 OM protein - protein search, using sw model
 Run on: April 6, 2004, 14:05:54 ; Search time 17 seconds
 (without alignments)
 1001.585 Million cell updates/sec

Title: US-09-787-844-2
 Perfect score: 1792
 Sequence: 1 RRGGRQAAGEANGARGAL.....PSWLLFPFLWALPLLPV 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	96.4	314	1	TEST HUMAN
2	1147	64.0	324	1	Q9Y6M0 mus musculus
3	603	33.6	321	1	Q9HJ77 mus musculus
4	580	32.4	343	1	Q9HJ77 mus musculus
5	574	32.0	290	1	Q9HJ77 mus musculus
6	562.5	31.4	342	1	Q9HJ77 mus musculus
7	561.5	31.3	342	1	Q9HJ77 mus musculus
8	556.5	31.1	311	1	Q9HJ77 mus musculus
9	544	30.4	273	1	Q9HJ77 mus musculus
10	543	30.3	811	1	Q9HJ77 mus musculus
11	531.5	29.7	317	1	Q9HJ77 mus musculus
12	528.5	29.5	270	1	Q9HJ77 mus musculus
13	522	29.1	275	1	Q9HJ77 mus musculus
14	520	29.0	306	1	Q9HJ77 mus musculus
15	515	28.7	275	1	Q9HJ77 mus musculus
16	514.5	28.7	638	1	Q9HJ77 mus musculus
17	514	28.7	275	1	Q9HJ77 mus musculus
18	513	28.6	638	1	Q9HJ77 mus musculus
19	512	28.6	276	1	Q9HJ77 mus musculus
20	511	28.5	275	1	Q9HJ77 mus musculus
21	511	28.5	638	1	Q9HJ77 mus musculus
22	509.5	28.4	273	1	Q9HJ77 mus musculus
23	509	28.4	811	1	Q9HJ77 mus musculus
24	508.5	28.4	454	1	Q9HJ77 mus musculus
25	507	28.3	273	1	Q9HJ77 mus musculus
26	505	28.2	453	1	Q9HJ77 mus musculus
27	500	27.9	274	1	Q9HJ77 mus musculus
28	499	27.8	275	1	Q9HJ77 mus musculus
29	490.5	27.4	435	1	Q9HJ77 mus musculus
30	489.5	27.3	418	1	Q9HJ77 mus musculus
31	487.5	27.2	455	1	Q9HJ77 mus musculus
32	483.5	27.0	625	1	Q9HJ77 mus musculus
33	478	26.7	437	1	Q9HJ77 mus musculus

ALIGNMENTS

RESULT 1

ID	TEST HUMAN	STANDARD;	PRT;	314 AA.
AC	Q9Y6M0; Q9NG34; Q9P2V6;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Testisin precursor (EC 3.4.21.-) (Eosinophil serine protease 1) (ESP-1) (UNQ266/PRO303).			
DE	1) (UNQ266/PRO303).			
GN	PRSS21 OR TEST1 OR ESP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Eosinophil;			
RX	MEDLINE=99045401; PubMed=9826525;			
RA	Inoue M., Kanbe N., Kurosawa M., Kido H.;			
RT	"Cloning and tissue distribution of a novel serine protease esp-1 from human eosinophils.";			
RL	Biochem. Biophys. Res. Commun. 252:307-312(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RX	MEDLINE=20068805; PubMed=10600542;			
RA	Inoue M., Isebe M., Itoyama T., Kido H.;			
RT	"Structural analysis of esp-1 gene (PRSS 21).";			
RL	Biochem. Biophys. Res. Commun. 266:564-568(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Cervical carcinoma;			
RX	MEDLINE=99323395; PubMed=10397266;			
RA	Hooper J.D., Nicol D.L., Dickinson J.L., Byre H.J., Scarman A.L.,			
RT	Normyle J.F., Stutgen M.A., Douglas M.L., Loveland K.A.,			
RL	Sutherland G.R., Antalis T.M.;			
RT	"Testisin, a new human serine proteinase expressed by premeiotic testicular germ cells and lost in testicular germ cell tumors.";			
RL	Cancer Res. 59:3199-3205(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20461760; PubMed=11004480;			
RA	Hooper J.D., Bowen N., Marshall H., Cullen L.M., Seod R., Daniels R.,			
RT	Stutgen M.A., Normyle J.F., Higgs D.R., Kastner D.L., Ogbourne S.M.,			
RL	Pera M.F., Jazwinska E.C., Antalis T.M.;			
RT	"Localization, expression and genomic structure of the gene encoding the human serine protease testisin.";			
RL	Biochim. Biophys. Acta 1492:63-71(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=2887296; PubMed=12975309;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RT	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RL	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heidens S.,			
RT	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RL	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RT	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			

34 477.5 26.6 417 1 HEP5 HUMAN
 35 472.5 26.4 422 1 DES1 HUMAN
 36 468 26.1 430 1 TMS2_MOUSE
 37 466 26.0 436 1 HEP5_MOUSE
 38 459.5 25.6 492 1 TMS2_HUMAN
 39 457.5 25.5 457 1 TMS5_HUMAN
 40 455.5 25.4 415 1 ACRO_PIG
 41 455.5 25.4 810 1 PLMN HUMAN
 42 454.5 25.4 1069 1 ENTK_MOUSE
 43 454 25.3 338 1 PLMN_HORSE
 44 452.5 25.3 436 1 ACRO_MOUSE
 45 447 24.9 416 1 HEP5_RAT

P05981 homo sapien
 Q9U152 homo sapien
 Q9J1Q8 mus musculus
 C35453 mus musculus
 Q15393 homo sapien
 Q9H363 homo sapien
 P08001 sus scrofa
 P00747 homo sapien
 P97435 mus musculus
 P80010 equus caball
 P23578 mus musculus
 Q05511 rattus norv

RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 CC -!- FUNCTION: Could regulate proteolytic events associated with
 CC testicular germ cell maturation.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=L;
 CC IsoId=Q9Y6M0-1; Sequence=Displayed;
 CC Name=2; Synonyms=S;
 CC IsoId=Q9Y6M0-2; Sequence=VSP_005389;
 CC Name=3;
 CC IsoId=Q9Y6M0-3; Sequence=VSP_005390;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in premeiotic
 CC testicular germ cells, mostly late pachytene and diplotene
 CC spermatocytes.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -----
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 CC -----
 CC EMBL; AF058300; AAD41588.1; -;
 CC EMBL; AB031329; BAA83520.1; -;
 CC EMBL; AB031330; BAA83521.1; -;
 CC EMBL; AB031331; BAA83522.1; -;
 CC EMBL; AF058301; AAF79019.1; -;
 CC EMBL; AF058302; AAF79020.1; -;
 CC EMBL; AY359034; AAQ89393.1; -;
 CC HSSP; P00763; LDPO.
 CC MEROPS; S01.011; -;
 CC Genew; HGNC:9485; PRSS21.
 CC MIM; 608159; -;
 CC GO; GO:0005737; C:cytoplasm; TAS.
 CC GO; GO:0005624; C:membrane fraction; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
 CC InterPro; IPR009003; Cys Ser trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS02040; TRYP_SIN_DOM; 1.
 CC PROSITE; PS00134; TRYP_SIN_HIS; 1.
 CC PROSITE; PS00135; TRYP_SIN_SER; 1.
 CC Hydrolase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen;
 KW Alternative splicing; Lipoprotein.
 KW SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 41
 FT CHAIN 42 288
 FT PROPEP 289 314
 FT ACT_SITE 82 82
 FT ACT_SITE 137 137
 FT ACT_SITE 238 238
 FT ACT_SITE 33 157
 FT DISULFID 67 83
 FT DISULFID 171 244
 FT DISULFID 204 223
 FT DISULFID 234 262
 FT DISULFID 288 288
 FT LIPID 167 200
 FT CARBOHYD 200

FT CARBOHYD 273 273 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 87 88 Missing (in isoform 2).
 FT FTid=VSP_005389.
 FT VARSPLIC 222 235 Missing (in isoform 3).
 FT FTid=VSP_005390.
 SQ SEQUENCE 314 AA; 34884 MW; E738CF73F6B56E98 CRC64;
 Query Match 96.4%; Score 1728; DB 1; Length 314;
 Best Local Similarity 100.0%; Pred.NO.1.2e-147; Indels 0; Gaps 0;
 Matches 314; Conservative 0; Mismatches 0;
 QY 14 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAELGRWPWGSLR 73
 DB 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAELGRWPWGSLR 60
 QY 74 LWDHVCVSVLLSHRWALTAHCFETYSDDLSDPSGVMVQGLTSMPSFWSLQAYTYRF 133
 DB 61 LWDHVCVSVLLSHRWALTAHCFETYSDDLSDPSGVMVQGLTSMPSFWSLQAYTYRF 120
 QY 134 VSNYLSPRYLGNSPYDIALVKLSAPVYTYKHQICLOASTFFENRTDCWVTGWGIK 193
 DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTYKHQICLOASTFFENRTDCWVTGWGIK 180
 QY 194 EDEALPSHTLQEVQVVAIINNSMCNHLFLKYSFKDIFGDMVCAGNAGGKDAFCGDSGG 253
 DB 181 EDEALPSHTLQEVQVVAIINNSMCNHLFLKYSFKDIFGDMVCAGNAGGKDAFCGDSGG 240
 QY 254 PLACNKGWLQIGVSWGVCGRPNRPVGVVYTNISHFEWIKLMAQSGMSQPPSPWLL 313
 DB 241 PLACNKGWLQIGVSWGVCGRPNRPVGVVYTNISHFEWIKLMAQSGMSQPPSPWLL 300
 QY 314 FFPLLWALPLLPV 327
 DB 301 FFPLLWALPLLPV 314
 RESULT 2
 TEST MOUSE STANDARD; PR7; 324 AA.
 ID TEST MOUSE AC Q9JHJ7; Q9DA14;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Testisin precursor (EC 3.4.21.-) (Trypsinase 4).
 GN PRSS21.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=21153229; PubMed=11231276;
 RA Scarnan A.L., Hooper J.D., Boucatt K.J., Sit M.-L., Webb G.C.,
 RA Normyle J.F., Antalio T.M.;
 RT "Organization and chromosomal localization of the murine Testisin gene
 RT encoding a serine protease temporally expressed during
 RT spermatogenesis.";
 RL Eur. J. Biochem. 268:1250-1258(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C; TISSUE=Testis;
 RX PubMed=11259427;
 RA Wong G.W., Li L., Madhusudhan M.S., Krilis S.A., Gurish M.F.,
 RA Rothenberg M.E., Sali A., Stevens R.L.;
 RT "Trypsinase 4, a new member of the chromosome 17 family of mouse serine
 RT proteases.";
 RL J. Biol. Chem. 276:20648-20658(2001).
 RN [3]
 RP SEQUENCE OF 3-324 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Ozaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glssi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wegner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga T., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Togo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Hayashizawa A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- FUNCTION: Could regulate proteolytic events associated with
CC testicular germ cell maturation.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- DEVELOPMENTAL STAGE: Expressed in post-meiotic testicular germ
CC cells.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a stop
CC codon in position 315.
CC -----
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CC -----
DR EMBL; AF304012; AAK29360.1; -;
DR EMBL; AY005145; AAG02255.1; -;
DR EMBL; AF176209; AAF64407.2; -;
DR EMBL; AF226710; AAF64428.2; -;
DR EMBL; AK006271; -; NOT_ANNOTATED_CDS.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.011; -;
DR MGD; MGI:1916698; Prrs21.
DR GO; GO:0005624; C-membrane fraction; IDA.
DR GO; GO:0004252; F-serine-type endopeptidase activity; IDA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen;
KW Lipoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 54 POTENTIAL.
FT CHAIN 55 298 TEST-SIN.
FT PROPEP 299 324 REMOVED IN MATURE FORM (POTENTIAL).
FT ACT_SITE 95 95 CHARGE RELAY SYSTEM (POTENTIAL).
FT ACT_SITE 147 147 CHARGE RELAY SYSTEM (POTENTIAL).
FT ACT_SITE 248 248 CHARGE RELAY SYSTEM (POTENTIAL).
FT DISULFID 46 167 POTENTIAL.
FT DISULFID 80 96 POTENTIAL.
FT DISULFID 181 254 POTENTIAL.
FT DISULFID 214 233 POTENTIAL.
FT DISULFID 244 272 POTENTIAL.
FT LIPID 298 298 GPI-anchor amidated asparagine
FT (Potential).
FT

FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 275 275 P -> H (IN REF. 3).
SQ SEQUENCE 324 AA; 36175 MW; 56DC59B84F3C3CD4 CRC64;
Query Match 64.0%; Score 1147; DB 1; Length 324;
Best Local Similarity 64.7%; Pred. No. 1.6e-95;
Matches 211; Conservative 39; Mismatches 60; Indels 16; Gaps 4;
QY 14 MGARGALLALL--LAPAGL-----RKPSQEAAPLSPGCGRRVITSRIVGGD 60
DB 1 MGARGKTLVPLVVVATAAALQSTLYQVDPEKPELQEPDLSGPGCHRTIPSRIVGGD 60
QY 61 AEIGRWPGQSLRWDSHVGVLLSHRWALTAHCFETYSDLSDSGWNVQGGITMP 120
DB 61 AEIGRWPGQSLRWGNHLCATLNRWVLTAAHCFQ--KD--NDPFDVTQVQELTSRP 117
QY 121 SFWSLQAYTRYFVSNIYLSPRYLGNSPYDIALVKLSAPVYTKHTQICLQASTPEFEN 180
DB 118 SLNWLQAYSNRYQIEDIFLSPKISEQYFNIDIALKLSPPVYNNFIQICLLNSTYKEFN 177
QY 181 RTDCVWTGMYIKEDALPSPTLQVQVAIINNMCNHLFLKYSFRKDFGDMVCA 240
DB 178 RTDCVWTGMYIKEDALPSPTLQVQVAIINNMCNHLFLKYSFRKDFGDMVCA 237
QY 241 QGGKACFGDSGGPLACNKLWYQIGVSWGVCGRNRPVYTNISHHFEVQKLM 300
DB 238 EGGKACFGDSGGPLACDQDTVWYGVWSGVCGRNRPVYTNISHHFEVQKLM 297
QY 301 SGMSQDPSPPLFFFLWALPLGP 326
DB 298 NGLRPDPVPLLLFLTLAWASSLLRP 323
RESULT 3
TRYG HUMAN STANDARD; PRT; 321 AA.
AC Q9NR2; Q9C015; Q9NR08; Q9UB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trypsin gamma precursor (EC 3.4.21.-) (transmembrane trypsinase).
GN TP8G1 OR TMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
RX MEDLINE=20302813; PubMed=10843716;
RA Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaro M.,
RA Wolters P.J., Verghese G.M.;
RT "Characterization of human gamma-tryptases, novel members of the
RT chromosome 16p mast cell tryptase and proctasin gene families.";
RL J. Immunol. 164:16566-16575(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99452974; PubMed=10521469;
RA Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA Friend D.S., Krilis S.A., Stevens R.L.;
RT "Identification of a new member of the tryptase family of mouse and
RT human mast cell proteases which possesses a novel COOH-terminal
RT hydrophobic extension.";
RL J. Biol. Chem. 274:30784-30793(1999).
RN [3]
RP SEQUENCE OF 220-321 FROM N.A.
RA Mittman S., Agnew W.S.;
RT "Organization and alternative splicing of CACNAH.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in many tissues.

CC cells. In the prostate gland it may be synthesized in epithelial
 CC cells, secreted into the ducts, and excreted into the seminal
 CC fluid.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -----
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 CC EMBL; L41351; AAC41759.1; -;
 CC EMBL; U33446; AAB19071.1; -;
 CC EMBL; BC001462; AAH01462.1; -;
 CC PIR; A57014; A57014.
 CC HSP; P00763; LDPO.
 CC MEROPS; S01.159; -;
 CC Genew; HGNC:9491; PRSS8.
 CC MIM; 600823; -;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0005886; C:plasma membrane; TAS.
 CC GO; GO:0008236; F:serine-type peptidase activity; TAS.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PRO0722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS02040; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC HydroLase; Serine protease; Zymogen; Signal; Glycoprotein;
 KW Transmembrane.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 32 ACTIVATION PEPTIDE.
 FT CHAIN 33 44 PROSTATIN LIGHT CHAIN.
 FT CHAIN 45 322 PROSTATIN HEAVY CHAIN.
 FT PROPEP 323 343 POTENTIAL.
 FT TRANSMEM 320 340 POTENTIAL.
 FT DOMAIN 45 286 SERINE PROTEASE.
 FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 70 86 BY SIMILARITY.
 FT DISULFID 168 244 BY SIMILARITY.
 FT DISULFID 201 223 BY SIMILARITY.
 FT DISULFID 234 262 BY SIMILARITY.
 FT ACT_SITE 85 85 CHARGE RELAY SYSTEM.
 FT ACT_SITE 134 134 CHARGE RELAY SYSTEM.
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM.
 FT CARBOHYD 159 159 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 343 AA; 36431 MW; 98DD6447F5A8C1B2 CRC64;
 Query Match 32.4%; Score 580; DB 1; Length 343;
 Best Local Similarity 40.6%; Pred. No. 1.3e-44;
 Matches 146; Conservative 47; Mismatches 107; Indels 60; Gaps 14;
 QY 3 ORGROAAGEAMGARGALLALLARAGLRKPESEAPLSPGCGRRVITSGVGEDAE 62
 DB 3 QKGVLPQO-ICA-VAIILYLGLRSG-TGAEGR-PCG-VAPOARITGSSAV 52
 QY 63 LGRWPMQGLRLWDHVGCVSLSHRWALTAAFCFETVSDLSPPS-----GMVQFG-Q 115
 DB 53 AGQWPQVQSVITGVHVCGLSVSEQVLSAAHCF-----PSEHKEAYEVKLGAAHQ 104
 QY 116 LNSMPSFSLQAVYTRYFVSNLYLSPRYL-GNSPVDIALVKLSAPVYTKHQPTCLQAS 174
 DB 105 LDS-----YSEDKAVST-LKDIIPHSYLOEQSGDIALQSRITFSRIVRIPCIPAA 158
 QY 175 TFEFENRTDWTGWYGIKEALSPHTLOEVQVAIINNSMCHLF---LKYSRKDF 231
 DB 159 NASFPNGLHCTVTGWGHVAPSVSLTPKPLQQLQEVPLISRETNCNLYNIDAKPEEPHFVQ 218

QY 232 GDMVCAAGNAQGGKACFGDSGGPLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHF 291
 DB 219 EDMVCAGYVEGGKACQGGSGPLSCPVEGLWYLGIVSGDACGARNRPGVYTLASSVA 278
 QY 292 EMTQ-----KLMAQSGMSQDPDSW-----PLLPPLWALPLLP 326
 DB 279 SWIQSVTELOPRVVPQTESQPSDNLGSHLAFSSAPAGLRPLFLPLGLGLGLSP 338
 RESULT 5
 PR27_HUMAN STANDARD; PRT; 290 AA.
 ID PR27_HUMAN Q9BQR3;
 AC Q9BQR3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pancreas precursor (EC 3.4.21.-) (Marapsin) (Channel-activating
 DE protease 2) (CAH2).
 GN PRSS27 OR MEN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.;
 RT "Cloning, sequencing and expression of marapsin, a human serine
 RT proteinase";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Okaze H., Hayashi A., Kozuma S., Saito T.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22439795; PubMed=12441343;
 RA Bhagwandin V.J., Hau L.W.-T., Mallen-St Clair J., Wolters P.J.,
 RA Caughey G.H.;
 RT "Structure and activity of human pancreas, a novel tryptic serine
 RT peptidase expressed primarily by the pancreas";
 RL J. Biol. Chem. 278:3363-3371(2003).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in the pancreas.
 CC -!- PTM: N-glycosylated.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ306593; CAC35467.1; -;
 CC EMBL; AB056161; BAB85497.1; -;
 CC EMBL; AY030095; AAK38168.1; -;
 CC HSP; P00734; IUVS.
 CC MEROPS; S01.074; -;
 CC Genew; HGNC:15475; PRSS27.
 CC MIM; 608018; -;
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PRO0722; CHYMOTRYPSIN.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS02040; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 KW HydroLase; Serine protease; Zymogen; Signal; Glycoprotein.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 34 POTENTIAL.

FT CHAIN 35 290 PANCREASIN.
FT DOMAIN 35 277 SERINE PROTEASE.
FT ACT_SITE 75 75 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 229 229 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 158 235 BY SIMILARITY.
FT DISULFID 191 214 BY SIMILARITY.
FT DISULFID 225 253 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 290 AA; 31940 MW; 67BDC93EC70BFF7B CRC64;

Query Match 32.0%; Score 574; DB 1; Length 290;
Best Local Similarity 42.8%; Pred. No. 3.7e-44;
Matches 123; Conservative 44; Mismatches 100; Indels 22; Gaps 8;

QY 17 RGALLALLARAGLRKPSQEAAPLSGPGSRVITSRIVGDEDAELGRWPQGSRLRWD 76
Db 3 RPAAPVLLLLLCFGSQRAKATA-----CGRPMLENRVVGQDTQEGENPQVSIQNG 56

QY 77 SHVGVSLSHRWALTAHCFETYSDLPDSGMVQFG--QLTSMPSFWSLOAYTRYFV 134
Db 57 SHPCGSLIAEQWVLTAAHCFER---NTSETSLYQVLLGARQLVQP-----GPHAMVYAR--V 107

QY 135 SNLYLSPRYLGN-SPYDIALVKLSAPVYTKHIQIQLQASTFEPENRDTDCWVTGWGVIK 193
Db 108 RQVESNPLVQGTASSADVALVEAPVPTNYILPVCLPDPSPVETGMNCHWTGWSPS 167

QY 194 EDALPSPTLQEVQVAIINNSMCHFLK---YSFR-KDIFGDMVCAGNAOGKDACFG 249
Db 168 EEDLLPEPRILQKLVPIIDTPKCNLLYSKDTFEGYQPKTKINDMLCAGFEGKDKACKG 227

QY 250 DSGGGLACNKGWYQIGVGVSWGCGRPNRPGVYTNISHHFEWIKLM 298
Db 228 DSGGGLVCLVQGSWQVLSWEGCGARQNPQVYIRVTAHNWIRHII 276

RESULT 6
PSS8 RAT
ID PSS8 RAT STANDARD; PRT; 342 AA.
AC Q9ES8; Q9ER01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Proctasin precursor (SC 3.4.21.-).
GN PSS8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Adachi M., Kitamura K., Miyoshi T., Tomita K.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA Wang C.;
RL Moleculer cloning and expression of rat proctasin.";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Possesses a trypsin-like cleavage specificity (By similarity).
CC -1- SUBUNIT: Heterodimer of two chains, light and heavy, held by a disulfide bond (By similarity).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC
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EMBL; AB017638; BAB20281.1; -;
EMBL; AF202076; AAC32641.1; -;
HSP; P00734; IUVS
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMC0020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
KW Transmembrane.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 32 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 33 44 PROSTATIN LIGHT CHAIN.
FT CHAIN 45 322 PROSTATIN HEAVY CHAIN.
FT PROPEP 323 342 BY SIMILARITY.
FT TRANSMEM 320 340 POTENTIAL.
FT DOMAIN 45 286 SERINE PROTEASE.
FT DISULFID 37 154 INTERCHAIN (BY SIMILARITY).
FT DISULFID 70 86 BY SIMILARITY.
FT DISULFID 168 244 BY SIMILARITY.
FT DISULFID 201 223 BY SIMILARITY.
FT DISULFID 234 262 BY SIMILARITY.
FT ACT_SITE 85 85 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 134 134 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 17 17 I -> V (IN REF. 1).
FT CONFLICT 292 292 A -> V (IN REF. 1).
SQ SEQUENCE 342 AA; 36843 MW; 5EDIAF0SD9213B98 CRC64;

Query Match 31.4%; Score 562.5; DB 1; Length 342;
Best Local Similarity 38.1%; Pred. No. 4.9e-43;
Matches 131; Conservative 53; Mismatches 93; Indels 67; Gaps 11;

QY 20 LLLALLARAGLRKPSQEAAPLSGPGSRVITSRIVGDEDAELGRWPQGSRLRWD 79
Db 19 LLIGLQSRIG---ADGTEAS-----CG-AVIFRITGGSAKPGQWPQVSIYNGVHV 69

QY 80 CGVSLSHRWALTAHCFETYSDLPDSGMVQFG--QLTSMPSFWSLOAYTRYFVSN- 136
Db 70 CGGSLVSNQWVWSAAHCFPREHSKEE--YEVKLGARHQLDSF-----SND 111

QY 137 --IVLSPRYLGNSPY-----DIALVKLSAPVYTKHIQIQLQASTFEPENRDTDCWVT 187
Db 112 IVVHTVAQIISHSYREEGSGDDIALRLSSPVTFSSYIRIPICLPAANAFPNGLHCTVT 171

QY 188 GWGIKEDALPSPTLQEVQVAIINNSMCHFLKYSFRK---IFGDMVCAGNAOGK 244
Db 172 GWGHVAPSVLSQTPRPLQQLLEVLPLISRETCSCLYNINAVPEEPTIQDMLCAGYVKGK 231

QY 245 DACFGDSGGPLACNKGWYQIGVGVSWGCGRPNRPGVYTNISHHFEWIK------K 296
Db 232 DACQDSGGPLSCPIDGLWYLAGIVSWGDACGAPNREGVYTLTSTYASWIIHHVAELQPR 291

QY 297 LMAQSGMSQDPP-----SWPLFFPPLLWALPL 323
Db 292 AVPTQESQDPGHLCHNHHPVFNLAQAQKLSRPLFLPLSLTLGL 335

RESULT 7
PSS8 MOUSE
ID PSS8 MOUSE STANDARD; PRT; 342 AA.
AC Q9RSD1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF175760; AAF03698.1; -
DR EMBL; AF175523; AAF03696.1; -
DR EMBL; BC052325; AAH52325.1; -
DR HSP; P20231; IAAO.
DR MEROPS; S01.028; -
DR MGD; MGI11349391; Tpsgl.
DR InterPro; IPR009003; Cys_Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE NEG.
KW Hydroxylase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Transmembrane.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 28 TRYPTASE GAMMA LIGHT CHAIN.
FT CHAIN 30 311 TRYPTASE GAMMA HEAVY CHAIN.
FT TRANSMEM 277 297 POTENTIAL.
FT ACT_SITE 70 70 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 117 117 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 18 137 INTERCHAIN (POTENTIAL).
FT DISULFID 55 71 BY SIMILARITY.
FT DISULFID 151 220 BY SIMILARITY.
FT DISULFID 184 202 BY SIMILARITY.
FT DISULFID 210 238 BY SIMILARITY.
FT CARBOHYD 77 77 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 311 AA; 7FC9D6BF6A2A8808 CRC64;

Query Match 31.1%; Score 556.5; DB 1; Length 311;
Best Local Similarity 39.8%; Pred. No. 1.5e-42;
Matches 132; Conservative 39; Mismatches 102; Indels 59; Gaps 10;

Qy 13 AMGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRTVGGEDAEIGRPWQGSGL 72
Db 2 ALGNCGL-LFLAVSGCGHPQVNSG-----SRVGGHAPAGTWPQASL 47
Qy 73 RLMDSHVGVGLLSHRWALTAACHFETYSYDLSPSGMMVQFGLTSPMSFWSLQAYTRY 132
Db 48 RLKHVHVCGSLSPWVLTAAHCFSGVNSSD---YQVHLGELT----- 89
Qy 133 FVSNIVLSR-----YLGN-----SPYDALVKLSAPVYVTKHIQICLQASTPEF 178
Db 90 ----VTLSPHSTVKRIIMVTGPGPGSGDIALVQLSPVALSQGVPCVLPESADP 145
Qy 179 ENRTDCVWTGMYIKEDALPSPTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAG 238
Db 146 YPGMQCVWTGMYTGEPEPLKPPYLNQEAQVSVVVKVTCQAVNSPN-GSLIQDMLC-- 202
Qy 239 NAQGGKACFCDSGGPLACKNGIWLQIGVYSGVGGCRNRRGVVNTISHHPEWIKLM 298
Db 203 -ARGPGDACQDSDGGLVQVAGTGWQAGVYVSGEGCRDPRGVTVARVYVNVNHHH 261
Qy 299 AQSGMS--QPDPSWPL---LFFPLLMALPLLG 325
Db 262 PEAGSGMQGLPWPAPLLAALFWPSLFLLVSG 293

RESULT 9
TRYT_SHEEP

ID TRYT_SHEEP STANDARD; PRT; 273 AA.
AC Q9XSM2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsase 2 precursor (BC 3.4.21.59).
OS Ovis aries (Sheep).
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Abomasum;
RX MEDLINE=20308142; PubMed=10848900;
RA Pemberton A.D., McLeese S.M., Huntley J.F., Collie D.D.S.,
RA Scudamore C.L., McQueen A.R., Walls A.F., Miller H.R.P.;
RT "cDNA sequence of two sheep mast cell trypsinase and the differential
RT expression of trypsinase and sheep mast cell proteinase-1 in lung,
RT dermis and gastrointestinal tract.";
RT Clin. Exp. Allergy 30:818-832(2000).
CC -!- FUNCTION: Trypsinase is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|- , Lys-|- , but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y18224; CAB41989.1; -
DR HSP; P20231; IAAO.
DR MEROPS; S01.143; -
DR InterPro; IPR009003; Cys_Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Signal; Glycoprotein; Zymogen.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 28 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 29 273 TRYPTASE 2.
FT ACT_SITE 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 57 73 BY SIMILARITY.
FT DISULFID 153 228 BY SIMILARITY.
FT DISULFID 186 209 BY SIMILARITY.
FT DISULFID 218 246 BY SIMILARITY.
FT CARBOHYD 231 231 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 273 AA; 30288 MW; D59BA79218C3E67D CRC64;

Query Match 30.4%; Score 544; DB 1; Length 273;
Best Local Similarity 40.5%; Pred. No. 1.7e-41;
Matches 118; Conservative 46; Mismatches 93; Indels 34; Gaps 10;

Qy 20 LLLALLARAGLRKPESQEAAPLSGPGRRVITSRTVGGEDAEIGRPWQGSRLWDS-- 77
Db 5 LALLALLSLV-----SAPAPQALQR---SGIIGKEAPGSRPWPQVSLVRDQYW 53


```

DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane;
FT GLYCOPROTEIN.
FT DOMAIN 1 59 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 60 80 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 81 811 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 213 336 CUB 1.
FT DOMAIN 323 440 CUB 2.
FT DOMAIN 445 477 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 478 514 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 518 555 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 565 799 SERINE PROTEASE.
FT ACT_SITE 617 617 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 668 668 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 518 518 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 690 690 P -> PP (IN REF. 2).
SQ SEQUENCE 811 AA; 90978 MW; 32EB3E7C3127801B CRC64;

Query Match
Best Local Similarity 30.3%; Score 543; DB 1; Length 811;
Matches 105; Conservative 41.2%; Pred. No. 7.3e-41;
Indels 14; Gaps 7;

QY 46 CGRVITSRVIGEDAEGLRWPGQSLRLWDSHVGVLSLHRAWLTAACHFTYSDLSL 105
DB 568 CGLGLSSRRVGGTVSGEGWPQASLQIRGHICGGLIADRWVTAACHFQEDS-MAS 626
QY 106 PSMVMVQFGLTSMPSFSLQAVYTRVFNIVLSRYLGNLS-PYDIALVKLSAPVYTK 164
DB 627 PCLWTVFLGKM-RQNSRPGEVSEFK---VSRFLHPHYHEEDSHDYDVALQLDHPVYGA 682
QY 165 HIQICLQASTFFENRTDCWVTGWYIKEDALPSPHTLQEVQVAINNSMCMHLFLKY 224
DB 683 TVRPVCLPARSHFPQCHCWITGWG--AQREGPVSNLTQKVDQLVQDLGSE----- 735
QY 225 SFRKDIFDGMVVCAGNAGGKDACFGDSGGFLGNK-NGLMYQIGVYGVWGCGRNPFGV 283
DB 736 AYRYQVSPMLCAGRYKGDACQGDGGGLVCRFPGRFLAGLVSWGLGCGRNPFGV 795
QY 284 YTNISHFBEWIKLM 298
DB 796 YTRVTRVINWQQVL 810

RESULT 11
BSS4 HUMAN STANDARD; PRT; 317 AA.
ID BSS4 HUMAN
AC Q9GZNA; O43342;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)
DE (SP001LA).
DE PRSS22 OR PRSS26 OR BSSP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsui S., Okui A., Kominami K., Yamaguchi N.;
RT "Cloning and characterization of a human brain-specific serine
protease, hBSSP-4."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

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```

RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Wong G.W., Stevens R.L.;
RT "Identification of a new member of the chromosome 16 family of serine
proteases."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22389257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 47-317 FROM N.A.
RA Ricke D.O., Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
RA Robinson D., Jones M., Buckingham J., Chasteen L., Thompson S.,
RA Goodwin L., Bryant J., Tesmer J., Meincke L., Longmire J., White S.,
RA Ueng S., Tatum O., Campbell C., Fawcett J., Deaven L.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC
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entities requires a license agreement (see http://www.ebi.ac.uk/announcements
or send an email to license@sib.ch).
CC
CC EMBL; AB010779; BAB20263.1; -
CC EMBL; AF321182; AAG35070.1; -
CC EMBL; BC009726; AA09726.1; -
CC EMBL; AC003965; AAB33671.1; -
CC HSP; P00763; LDPO.
CC MEROPS; S01.252; -.
CC Genew; HGNC:14368; PRSS22.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00085; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO0020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 317 BRAIN-SPECIFIC SERINE PROTEASE 4.
FT ACT_SITE 90 90 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 141 141 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 242 242 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 75 91 BY SIMILARITY.
FT DISULFID 175 248 BY SIMILARITY.
FT DISULFID 208 227 BY SIMILARITY.
FT DISULFID 238 266 BY SIMILARITY.

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```

FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ CONFLICT 47 L -> M (IN REF. 4).
FT SEQUENCE 317 AA; 33731 MW; E2A123BC86E79935 CRC64;

Query Match
Best Local Similarity 29.7%; Score 531.5; DB 1; Length 317;
Matches 111; Conservative 57; Mismatches 115; Indels 25; Gaps 6;

QY 15 GARGALLALLIARAGLRKPSQEAAPLSGPGRRVITSRVGGDEALGRWPWGQSLRL 74
DQ 13 GCLGFTFTSLLIATAAIL--NAARIPVPACPKPQQLNRVVGGEDSTDESWPVIISIQK 69
QY 75 WDSHVCVGLSHRWALTAHCFEYISDLSPSGMWVQFGLTSMPSFWSLQAYYTR-YF 133
DQ 70 NGTHCAGSLTTSRVITTAHCFK--DNINRYPYFVLLGA-----WQGNPGSRQK 120
QY 134 VSNYILSPR----YLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENETDCWVTGW 189
DQ 121 VGVAVPEHPVYVSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGW 180
QY 190 GYIKEDALPSPHTLQEVQVAIINNSMCHLFLKYSFKDIFGDMVCAGNAGGKDACFG 249
DQ 181 GSIQGVFLPHPTQIKUKVPIIDSEVCSHLYWRGAGQPTEDMWCAGYLEGERDACLG 240
QY 250 DSGGLACNKGWLWQIGVWSGVGCGRPNRPVYTNISHHFEWIKL-----AQK 301
DQ 241 DSGGLACNKGWLWQIGVWSGVGCGRPNRPVYTNISHHFEWIKL-----AQK 301
QY 302 GMSQPDPS 309
DQ 301 GMSQPDPS 308

RESULT 12
TRYT_PIG
ID TRYT_PIG STANDARD; PRT; 270 AA.
AC QN2D1;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast cell tryptase precursor (EC 3.4.21.59).
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGS/SEA; TISSUE=Intestine;
RX MEDLINE=95366971; PubMed=7639711;
RA Murakumo Y., Ide H., Itoh H., Tomita M., Kobayashi T.,
RA Maruyama H., Horii Y., Nawa Y.;
RT "Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil,
RT Meriones unguiculatus, and its preferential expression in the
RT intestinal mucosa."
RL Biochem. J. 309:921-926(1995).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
CC -----
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CC -----
DR EMBL; D31789; BAA06598.1; -.
DR PIR; S56160; S56160.
DR HSRP; P20231; IAAO.
DR MEROPS; S01.143; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.

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DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 270 MAST CELL TRYPTASE.
FT ACT_SITE 69 69 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 116 116 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 219 219 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 54 70 BY SIMILARITY.
FT DISULFID 150 225 BY SIMILARITY.
FT DISULFID 183 206 BY SIMILARITY.
FT DISULFID 215 243 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 270 AA; 30166 MW; 1BE102DB86943401 CRC64;

Query Match
Best Local Similarity 29.5%; Score 528.5; DB 1; Length 270;
Matches 118; Conservative 36; Mismatches 92; Indels 45; Gaps 9;

QY 20 LLLALLLALRAGLRKPSQEAAPLSGPGRRVITSRVGGDEALGRWPWGQSLR---LW 75
DQ 5 LLLALFLFSLMRSPLCQEWG-----IVGGQEAAPGNKWPQVSLRANETW 50
QY 76 DSHVCGVSLSHRWALTAHCFEYISDLSPSGMWVQFGLTSMPSFWSLQAYYTRYF-- 133
DQ 51 -RHFCGSLHHPQWLTAHNC--VGPTIADPNKRVQ-----LRQYLYYHDH 95
QY 134 ----VSNYILSPR-YLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENETDCWVTGW 189
DQ 96 LLAIVSRITHTPTFYATQNGADIALLELKNPVNISHHFEVSLPPASSETPPSGTLCWVTGW 155
QY 190 GYIKEDALPSPHTLQEVQVAIINNSMCHLFLKYSFKD---IFGDMVCAGNAGGKXD 245
DQ 156 GNIDNDVSLPPFPPLKEVQVPPVENCLDKYHKGYVTGDNHIVRDDMLCAGNE--GHD 213
QY 246 ACPGDSGGPLACNKGWLWQIGVWSGVGCGRPNRPVYTNISHHFEWIK 296
DQ 214 SCQDSSGGLGVCKVNGTWLQAGVWSNGEGCALPNRPGIYTRYTYLDWIHR 264

RESULT 13
TRYT_PIG
ID TRYT_PIG STANDARD; PRT; 275 AA.
AC QN2D1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptase precursor (EC 3.4.21.59).
GN MCT7.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung.
RX MEDLINE=20285343; PubMed=10824103;
RA Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,
RA Yano M., Yang B., Kido H.;
RT "Mast cell tryptase from pig lungs triggers infection by pneumotropic
RT Sendai and influenza A-viruses. Purification and characterization."
RL Eur. J. Biochem. 267:3189-3197(2000).
CC -!- FUNCTION: Tryptase is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.

```

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Released from the secretory granules upon
 CC mast cell activation.
 CC -1- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
 CC
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 CC
 CC EMBL; AB038652; BAA93614.1; -
 CC HSP; P20231; IAAO.
 CC MEROPS; S01.143; -
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00200; TRY_SPC; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KX Hydroxylase; Serine protease; Signal; Glycoprotein; Zymogen.
 CC FT SIGNAL 1 20 POTENTIAL
 CC FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
 CC FT CHAIN 31 275 TRYPTASE.
 CC FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 59 75 BY SIMILARITY.
 CC FT DISULFID 155 230 BY SIMILARITY.
 CC FT DISULFID 188 211 BY SIMILARITY.
 CC FT DISULFID 220 248 BY SIMILARITY.
 CC FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SQ SEQUENCE 275 AA; 30439 MW; ACC582647FCCB973 CRC64;
 CC
 CC Query Match 29.1%; Score 522; DB 1; Length 275;
 CC Best Local Similarity 42.7%; Pred. No. 1.6e-39;
 CC Matches 114; Conservative 34; Mismatches 93; Indels 26; Gaps 9;
 CC
 CC QY 40 APLSGCGRVITSRVGGDEALGRWPWGSLRLWD---SHVGVSLSHRWALTAHC 96
 CC DB 19 APAPGQALER---AGIVGKKEAPCHKWPQVSLRCLDQYWKHFCGSLHPQWLTAHC 75
 CC
 CC QY 97 FEIYSDLDSFGWMVQFGLTSPFWSLQAVY--TRYFVSNILSPRYLGN-SPYDIAL 153
 CC DB 76 FG--PEKADFLYTRVQLGE-----QHLYIQDRLLIVSRILVHPNYDEVNGADIAL 124
 CC
 CC QY 154 VKLSAPVYTKHIQICLQASTFEFNRTDCWVTGMYGKEDALPSHTLOEVQVAITN 213
 CC DB 125 LELEDPNLSHSHVQVTLPPASFTFKGTRCWVTGMDVHSGWLPPLPPYPLQVRVPIE 184
 CC
 CC QY 214 NSMCN---HLFLKYSRPKDIF-CDMKVCAGNAQGGKDACGDSGGPLACNKGWLQVGV 269
 CC DB 185 NSCEDMQYHGLSTGNIPVIRDMLCAGSE--GHDSCQDGGGGLVCRVNGTWLQAGVV 242
 CC
 CC QY 270 SWGVGCGRPNRPGVYTNISHFPEWIK 296
 CC DB 243 SWEGGALPNRPGIYTRVTHYLDWIHQ 269
 CC
 CC RESULT 14
 CC BSS4 MOUSE STANDARD; PRT; 306 AA.
 CC ID BSS4 MOUSE
 CC AC QSER10;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
 GN PRS22 OR PRS26 OR BSSP4.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_taxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Brain;
 CC RC
 CC Mitsu S., Okui A., Kominami K., Yamaguchi N.;
 CC "Cloning and characterization of a novel serine protease, mBSSP-4";
 CC SUBMITTED (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC
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 CC
 CC EMBL; AB010778; BAB20262.1; -
 CC HSP; P00763; IDPO.
 CC MEROPS; S01.252; -
 CC MGD; MGI:1918085; 4733401N09Rik.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00200; TRY_SPC; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KX Hydroxylase; Serine protease; Signal.
 CC FT SIGNAL 1 32 POTENTIAL.
 CC FT CHAIN 33 306 BRAIN-SPECIFIC SERINE PROTEASE 4.
 CC FT ACT_SITE 90 90 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 141 141 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 242 242 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 75 91 BY SIMILARITY.
 CC FT DISULFID 175 248 BY SIMILARITY.
 CC FT DISULFID 208 227 BY SIMILARITY.
 CC FT DISULFID 238 266 BY SIMILARITY.
 CC FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SQ SEQUENCE 306 AA; 33262 MW; FBBF03C0C285E7E8 CRC64;
 CC
 CC Query Match 29.0%; Score 520; DB 1; Length 306;
 CC Best Local Similarity 38.0%; Pred. No. 2.8e-39;
 CC Matches 113; Conservative 54; Mismatches 102; Indels 28; Gaps 7;
 CC
 CC QY 20 LLLALLARAGLRKPSQEAAPLSGPGRRVITSRVGGDEALGRWPWGSLRLWDVSHV 79
 CC DB 19 ILLVLLSTA---PISAATIRVPCGKPKQLNRIVGGSDMDAQWPWIVSLKNGSHH 74
 CC
 CC QY 80 CGVSLSHRWALTAHCFTETYSYDLSGPGWMVQFGLTSPFWSLQAVYTR---YFVSN 136
 CC DB 75 CAGSLNTRVWVTAACHCFK--SNMDKPSLFSVLGA-----WKLSPGPRSKYGVIAW 125
 CC
 CC QY 137 IYLSPRY--LQNSPYDIALVKLSAPVYTKHIQICLQASTFEFNRTDCWVTGMYGIKE 194
 CC DB 126 VLPHPRYSWKEGTHADIALVRLSHIQFSERILPICLPDSSVRLPPKTDGWIAGWSIQD 185
 CC
 CC QY 195 DEALPSPTHTLOEVQVAITNNSMCNHLFLKYSRPKDIFGDMVCAGNAQGGKDACGDSGGP 254
 CC DB 186 GVPLPFQTLQKLKVPIDSELCKSLYWRGAGQAEITEGMLCAGYLEGERDACLGGSGGP 245
 CC
 CC QY 255 LACNKGWLQVGVSWGVGCGRPNRPGVYTNISHFPEWIKL-----MAQSG 302
 CC DB 246 LMCQVDDHLLTGIISWEGCA--DDREGVYTSLLAHSRQVIRIVQGVQLGSLADSG 301

```
RESULT 15
TR1_HUMAN
ID Q15661; Q15663; Q9H2Y4; PRT; 275 AA.
AC Q15661; Q15663; Q9H2Y4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypsin beta-1 precursor (EC 3.4.21.59) (tryptase 1) (Trypsin I).
CN TP5B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90251647; PubMed=2187193;
RA Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA Caughey G.H.;
RT "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene
RT serine protease family";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=99121069; PubMed=9920877;
RA Pallao M., Fejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
RA Hattiarachi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA Hunt J.E.;
RT "Molecular cloning and characterization of novel human tryptase cDNAs
RT and solving variants";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Tryptase is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q15661-1; Sequence=displayed;
CC Name=2;
CC IsoId=Q15661-2; Sequence=VSP_005375;
CC -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
CC
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CC
CC EMBL; M33494; AAC83172.1; -
CC EMBL; M33491; AAA36778.1; -
CC EMBL; AF099144; AAD17860.1; -
CC EMBL; AF206667; AAC35697.1; -
CC PIR; A35863; A35863.
CC HSP; P20231; 1A0L.
CC MEROPS; S01.242; -.
CC Genew; HGNC:12019; TP5B1.
CC MIM; 191081; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
```

```
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Alternative splicing; Polymorphism.
FT SIGNAL 1 18
FT PROPEP 19 30
FT CHAIN 31 275
FT ACT_SITE 74 74
FT ACT_SITE 121 121
FT ACT_SITE 224 224
FT DISULFID 59 75
FT DISULFID 155 230
FT DISULFID 188 211
FT DISULFID 220 248
FT CARBOHYD 132 132
FT CARBOHYD 233 233
FT VARSPPLIC 79 87
FT VARIANT 18 18
FT VARIANT 23 23
FT VARIANT 85 85
FT VARIANT 132 132
FT VARIANT 141 141
FT VARIANT 162 162
FT VARIANT 170 170
FT VARIANT 215 215
FT VARIANT 216 216
FT SEQUENCE 275 AA; 30515 MW; ADC48FDC51F37112 CRC64;
Query Match 28.7%; Score 515; DB 1; Length 275;
Best Local Similarity 40.3%; Pred. No. 6.9e-39;
Matches 116; Conservative 42; Mismatches 92; Indels 38; Gaps 11;
QY 20 LLLAL--LLRAGLRKPEQEAAPLSGCGSRVITSIVGGEDAEELGRWPHQGSURL--- 74
Db 5 LLLALPVLASRA-----YAAPAQALQVR---GIVGGQAPRKRWPMQVSLRVHGP 53
QY 75 -WDGHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQLTSMPSFWSLQAYTRYF 133
Db 54 YW-NHFQGGSLIHPQWVLTAAHC--VGPDKVLAALRVQLRE-----QHLYYQDL 101
QY 134 --VSNIVLSR-VLGNSPYDIALVKLSAPVYTHYHQIQCLOASTFEFEFRNTDQWVGW 190
Db 102 LPVSRIVHPQFYTAQAGADALLEEPEPVNSHSHVHTVTLPPASETFPPGMPQWVTGW 161
QY 191 YIKDEALPSPHTLQEVQVAIINNMCNHLFLKYSFKD---IFGDMVCAAGAQGGKDA 246
Db 162 DVDNDRLLPFPPLKQVKVPIEMENHICDAKVLGAYTGDDVIRVDRDMLCAGNTR--RDS 219
QY 247 CFGDSGGFLACNKLWYQGVSVGWGCGRPNRPQGVYTNISHHFEWI 294
Db 220 CQDGGGGLVCKVNGTGLQAGVSWGEGCAQPNRPQGIYTRVYLDWI 267
Search completed: April 6, 2004, 14:12:06
Job time : 18 secs
```

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OM protein - protein search, using sw model

Run on: April 6, 2004, 14:05:19 ; Search time 59 Seconds
(without alignments)
1565.984 Million cell updates/sec

Title: US-09-787-844-2

Perfect score: 1792

Sequence: 1 RRGGRQAAGEAMGARGAL.....PSWLLFFLLWALPLGPV 327

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1792	100.0	327	3	AAY91871 Human can
2	1728	96.4	314	2	AAW77296 Amino aci
3	1728	96.4	314	2	AAW97116 A human e
4	1728	96.4	314	2	AAW97116 A human e
5	1728	96.4	314	2	AAY06434 Human pro
6	1728	96.4	314	2	AAY13388 Amino aci
7	1728	96.4	314	3	AAB12132 Hydrophob
8	1728	96.4	314	3	ADC78569 Human PRO
9	1728	96.4	314	4	AB80256 Human PRO
10	1728	96.4	314	4	AAU02223 Human ext
11	1728	96.4	314	5	AAE17010 Human eos
12	1728	96.4	314	6	ABU71634 Human PRO
13	1728	96.4	314	6	ABU71489 Human PRO
14	1728	96.4	314	6	ABU71935 Human sec
15	1728	96.4	314	6	ABO01818 Novel hum
16	1728	96.4	314	6	ABU54391 Human sec
17	1728	96.4	314	6	ABO47406 Human sec
18	1728	96.4	314	6	ABU67389 Human sec
19	1728	96.4	314	6	ABO14909 Human sec
20	1728	96.4	314	6	ABU69666 Novel hum
21	1728	96.4	314	6	ABO14848 Human sec
22	1728	96.4	314	6	ABD29462 Human sec
23	1728	96.4	314	6	ADA1818 Human sec
24	1728	96.4	314	6	ABO32800 Human sec
25	1728	96.4	314	6	ABO34860 Human PRO

26	1728	96.4	314	6	ADA16293 Human sec
27	1728	96.4	314	6	ADA42438 Human sec
28	1728	96.4	314	6	ABO17538 Human PRO
29	1728	96.4	314	7	ADA16717 Human sec
30	1728	96.4	314	7	ADA13146 Human sec
31	1728	96.4	314	7	ADA42014 Human sec
32	1728	96.4	314	7	ADA17361 Human sec
33	1728	96.4	314	7	ADA42864 Human sec
34	1728	96.4	314	7	ABO17599 Human PRO
35	1728	96.4	314	7	ADB80572 Ovarian c
36	1728	96.4	314	7	ADB77783 Human sec
37	1728	96.4	314	7	ADB74919 Human sec
38	1728	96.4	314	7	ADC28565 Human sec
39	1728	96.4	314	7	ADC39765 Human sec
40	1728	96.4	314	7	ADC40279 Human sec
41	1728	96.4	314	7	ADC19103 Human sec
42	1728	96.4	314	7	ADC34403 Human sec
43	1728	96.4	314	7	ADC29458 Human sec
44	1728	96.4	314	7	ADC38989 Human sec
45	1728	96.4	314	7	ADC40874 Human sec

ALIGNMENTS

RESULT 1

AY91871

ID AY91871 standard; protein; 327 AA.

XX AC AY91871;

XX AC AY91871;

DT 19-JUL-2000 (first entry)

DE Human cancer-specific gene protein, Prol04.

DE Human cancer-specific gene protein, Prol04.

XX Human cancer-specific gene protein; Prol04; serine protease; diagnosis;

XX Human cancer-specific gene protein; Prol04; serine protease; diagnosis;

KW staging; imaging; treating; gynecologic cancer; testicular cancer.

KW staging; imaging; treating; gynecologic cancer; testicular cancer.

XX Homo sapiens.

XX Homo sapiens.

OS Homo sapiens.

OS Homo sapiens.

PH Domain

PH Domain

FT Cleavage-site

FT Cleavage-site

FT Domain

FT Domain

XX /label= active_protease_domain

XX /label= active_protease_domain

XX /label= active_protease_domain

XX /label= active_protease_domain

XX /label= active_protease_domain

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XX /label= active_protease_domain

XX /label= active_protease_domain

XX /label= active_protease_domain

XX /label= active_protease_domain

XX /label= active_protease_domain

Methods for diagnosing, staging, imaging and treating gynecologic and testicular cancers by measuring expression of a cancer specific gene.

Example 2; Page 32-33; 36pp; English.

This protein sequence is encoded by human cancer-specific gene (CSG), Prol04. Prol04 is a serine protease that shares 31 percent homology with human hepsin at the amino acid level. When aligned with other serine proteases, Prol04 shares all the conserved amino acid motifs that are characteristic of all other serine proteases, in particular a highly conserved RIVGG sequence (see AAY91872). The inventive methods comprise

CC measuring expression of CSG in order to diagnose, stage, image and treat
 CC gynecologic and testicular cancers. The levels of CSG are compared to
 CC levels found in a normal human control (a change in the measured level of
 CC CSG is associated with the presence of the cancer). The early diagnosis
 CC of cancers improves the success rate of therapeutic protocols
 XX
 SQ Sequence 327 AA;

Query Match 100.0%; Score 1792; DB 3; Length 327;
 Best Local Similarity 100.0%; Pred. NO. 9.8e-154;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RRQRGAAGEEAMGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGED 60
 DB 1 RRQRGAAGEEAMGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGED 60
 QY 61 AELGRWPQCSRLRWDSHVCVSLLSHRWALTAHCFETYSDLSDFSGMWVQGLTSMF 120
 DB 61 AELGRWPQCSRLRWDSHVCVSLLSHRWALTAHCFETYSDLSDFSGMWVQGLTSMF 120
 QY 121 SFMSLQAYTRYFYVSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEEN 180
 DB 121 SFMSLQAYTRYFYVSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEEN 180
 QY 181 RTDCWVTGWYIKEDEALPSFHTLOEVQVAIIINNSMNCNHLFLKYSRDKIFGDMVCAGNA 240
 DB 181 RTDCWVTGWYIKEDEALPSFHTLOEVQVAIIINNSMNCNHLFLKYSRDKIFGDMVCAGNA 240
 QY 241 QGGKDCACFGDSGGPLACNKNGLWYQGVWSWGVCGRPNRPBGVYTNISHHFEWIOKLMAQ 300
 DB 241 QGGKDCACFGDSGGPLACNKNGLWYQGVWSWGVCGRPNRPBGVYTNISHHFEWIOKLMAQ 300
 QY 301 SGMSQDPPSWPLLPFLLWALPLLPV 327
 DB 301 SGMSQDPPSWPLLPFLLWALPLLPV 327

RESULT 2

AAW77296
 ID AAW77296 standard; protein; 314 AA.

XX AAW77296;

DT 07-JAN-1999 (first entry)

XX Amino acid sequence of the short isoform of HELA2.

XX Serine protease; regulation; cell activity; viability; HELA2; ATC2;
 KW BCOM3; testis; fertility; suppressor; testicular germ cell cancer;
 KW seminoma; testis-specific expression; antitumour; sperm development;
 XX infertility.

XX Homo sapiens.

XX WO9836054-A1.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-AU000085.

XX 13-FEB-1997; 97AU-00005101.

XX 18-NOV-1997; 97AU-00000422.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Antalis TM, Hooper JD;

XX WPI; 1998-480768/41.

XX N-PSDB; AAV59118.

XX New serine protease(s) and kinase involved in regulating cell activity
 PT and viability - particularly the testis-specific protease HELA2 used for
 PT modulation of fertility and as tumour suppressor.

XX

XX Claim 2; Fig 6; 167pp; English.

XX The present sequence represents the amino acid sequence of the short
 CC isoform of HELA2. cDNA generated from HeLa cells and PAI-2 expressing
 CC HeLa cells was amplified using PCR primers AAV48312-13. Three new
 CC sequences were detected in the 480 bp amplicon. These sequences are
 CC designated HELA2 and ATC2 which have high homology to serine proteases
 CC and BCOM3 which has homology to a kinase. The proteins are involved in or
 CC associated with regulation of cell activity and/or viability.
 CC Administration of recombinant HELA2 (also called testisin) is used to
 CC increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is
 CC also a suppressor of testicular germ cell cancers (seminoma) and is also
 CC expressed in some non-testicular cancers (of colon, pancreas, prostate
 CC and ovary), so is a marker/potential therapeutic target for cancer. The
 CC promoter from the HELA2 gene is useful for testis-specific expression of
 CC other genes, e.g. for gene therapy or modulation of fertility. Drugs that
 CC block activity of HELA2 should have antitumour activity (other than in
 CC testis) while in testis recombinant HELA2 should stop growth of tumours
 CC and normalise sperm development (eliminating the need for orchidectomy).
 CC Identification of mutant forms of HELA2 can be used to diagnose
 CC infertility

XX Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. NO. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGEDAEGLRWPQCSLR 73

DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCRRVITSRIYGGEDAEGLRWPQCSLR 60

QY 74 LWDSHVCVSLLSHRWALTAHCFETYSDLSDFSGMWVQGLTSMFSLQAYTRYF 133

DB 61 LWDSHVCVSLLSHRWALTAHCFETYSDLSDFSGMWVQGLTSMFSLQAYTRYF 120

QY 134 VSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEENRTDCWVTGWYIK 193

DB 121 VSNLYLSPRYLNSPYDIALVKLSAPVYTKHQICLOASTFEENRTDCWVTGWYIK 180

QY 194 EDEALPSFHTLOEVQVAIIINNSMNCNHLFLKYSRDKIFGDMVCAGNAQGGKDCACFGDSGG 253

DB 181 EDEALPSFHTLOEVQVAIIINNSMNCNHLFLKYSRDKIFGDMVCAGNAQGGKDCACFGDSGG 240

QY 254 PLACNKNGLWYQGVWSWGVCGRPNRPBGVYTNISHHFEWIOKLMAQSGMSQDPPSWPL 313

DB 241 PLACNKNGLWYQGVWSWGVCGRPNRPBGVYTNISHHFEWIOKLMAQSGMSQDPPSWPL 300

QY 314 FFPILLWALPLLPV 327

DB 301 FFPILLWALPLLPV 314

RESULT 3

AAW97116
 ID AAW97116 standard; protein; 314 AA.

XX AAW97116;

XX 04-MAY-1999 (first entry)

XX A human eosinophil serine protease.

XX Human; eosinophil; serine protease; allergic disease; infectious disease;
 KW tumour; granulomatous disease; collagen disease; vascular inflammation.

XX Homo sapiens.

XX JPI1032768-A.

XX 09-FEB-1999.

XX


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PF 16-JUL-1997; 97JP-00191319.
XX
PR 16-JUL-1997; 97JP-00191319.
XX
PA (ONOF) ONO PHARM CO LTD.
XX
DR WPI; 1999-193825/16.
DR N-PSDB; AAX15336.
XX
New eosinophils serine protease - useful for prevention and treatment of
PT allergic, infectious, tumor, granulomatous and collagen diseases.
XX
PS Claim 1; Page 9-10; 18pp; Japanese.
XX
CC The present sequence represents a human eosinophil serine protease. The
CC protease is useful in drug compositions for the prevention and treatment
CC of allergic diseases, infectious diseases, tumour diseases, granulomatous
CC diseases, collagen diseases and vascular inflammation
XX
SQ Sequence 314 AA;
Query Match 96.4%; Score 1728; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 73
Dd 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 60
QY 74 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPFSWLSIQAYTYTF 133
Dd 61 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPFSWLSIQAYTYTF 120
QY 134 VSNIVLSRYLGNISPYDIALVKLSAPVYTKHIQICLOASTFEFNRTDCWVTGWGIK 193
Dd 121 VSNIVLSRYLGNISPYDIALVKLSAPVYTKHIQICLOASTFEFNRTDCWVTGWGIK 180
QY 194 EDEALPSPTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAGGKDACFGDSGG 253
Dd 181 EDEALPSPTLQEVQVVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKGNGLWQIGVSVGVGCGRPNRGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 313
Dd 241 PLACNKGNGLWQIGVSVGVGCGRPNRGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
QY 314 FPELLWALPLLGPV 327
Dd 301 FPELLWALPLLGPV 314
RESULT 4
AAY06434
ID AAY06434 standard; protein; 314 AA.
AC AAY06434;
XX
XX 27-SEP-1999 (first entry)
XX Human protease HUPM-3.
XX
XX Protease; human; HUPM-3; cell proliferation; cancer; immune disorder;
XX inflammation; therapy.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1. 19
XX /note= "putative signal peptide"
XX Protein 20. 314
XX /note= "putative mature protein"
XX Modified-site 39
XX /note= "protein kinase C phosphorylation site"
XX Modified-site 58

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FT Modified-site /note= "protein kinase C phosphorylation site"
FT 73 /note= "protein kinase C phosphorylation site"
FT 82
FT Active-site 86
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 127
FT Modified-site /note= "protein kinase C phosphorylation site"
FT 134
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 161
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 167
FT Modified-site /note= "N-glycosylated"
FT 190
FT Modified-site /note= "casein kinase II phosphorylation site"
FT 200
FT Modified-site /note= "N-glycosylated"
FT 212
FT Modified-site /note= "protein kinase C phosphorylation site"
FT 238
FT Active-site 273
FT Modified-site /note= "N-glycosylated"
FT 291
FT Modified-site /note= "casein kinase II phosphorylation site"
FT W09936550-A2.
XX
XX 22-JUL-1999.
XX
XX 12-JAN-1999; 99MO-US000655.
XX
XX 16-JAN-1998; 98US-00008271.
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Hillman JL, Yue H, Guegler KJ, Corley NC, Tang YT;
XX Shah P;
XX WPI; 1999-430616/36.
XX N-PSDB; AAX87151.
XX
XX Novel human protease molecules useful in the treatment of developmental
XX disorders and/or cancers.
XX
XX Claim 1; Page 71-72; 90pp; English.
XX
XX The present sequence represents novel human protease HUPM-3, as deduced
XX from the consensus sequence (see AAX87151) of overlapping cDNA clones
XX obtained from various libraries. Northern analysis shows expression of
XX HUPM-3 in cardiovascular, haematopoietic and male reproductive cDNA
XX libraries. Approximately 86% of these libraries are associated with
XX neoplastic disorders. The invention provides 12 new human proteases, i.e.
XX HUPM-1 to -12 (see AAY06432-43), and the polynucleotides encoding them
XX (see AAX87149-60). Also provided are vectors, host cells and methods for
XX producing HUPM polypeptides, as well as agonists and antagonists of HUPM.
XX Methods for treating or preventing cell proliferative disorders and
XX immune disorders using HUPM or HUPM antagonists are claimed
XX
XX Sequence 314 AA;
Query Match 96.4%; Score 1728; DB 2; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 73
Dd 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGEDAEELGRWPQGSRLR 60
QY 74 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPFSWLSIQAYTYTF 133
Dd 61 LWDSHVCGVSLSHRWALTAACHCFETYSDLPSCGMVQFGOLTSMPFSWLSIQAYTYTF 120

```

QY 134 VSNLYSPRYLGNRPYDIALVKLSAPVTYTKHIQIPICLOASTFEFENRTDCWVTGWGYYK 193
 Db 121 VSNLYSPRYLGNRPYDIALVKLSAPVTYTKHIQIPICLOASTFEFENRTDCWVTGWGYYK 180
 QY 194 EDEALPSHTLQEQVVALINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 253
 Db 191 EDEALPSHTLQEQVVALINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 240
 QY 254 PLACNKNGLWYQIGVWSGVGCGRPNRPVYNTNSHFEWIKLMAQSGMSQDPDPSWPLL 313
 Db 241 PLACNKNGLWYQIGVWSGVGCGRPNRPVYNTNSHFEWIKLMAQSGMSQDPDPSWPLL 300
 QY 314 FPELLWALPLPGPV 327
 Db 301 FPELLWALPLPGPV 314
 RESULT 5
 AAY13388
 ID AAY13388 standard; protein; 314 AA.
 XX
 AC AAY13388;
 XX
 DT 25-JUN-1999 (first entry)
 XX
 DE Amino acid sequence of protein PRO303.
 XX
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX
 OS Homo sapiens.
 XX
 EN WO9914328-A2.
 XX
 PD 25-MAR-1999.
 XX
 FF 16-SEP-1998; 98WO-US019330.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 28-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.

29-OCT-1997; 97US-0063732P.
 29-OCT-1997; 97US-0063734P.
 29-OCT-1997; 97US-0063735P.
 29-OCT-1997; 97US-0063738P.
 29-OCT-1997; 97US-0064215P.
 31-OCT-1997; 97US-0063870P.
 31-OCT-1997; 97US-0064103P.
 03-NOV-1997; 97US-0064248P.
 07-NOV-1997; 97US-0064809P.
 12-NOV-1997; 97US-0065186P.
 17-NOV-1997; 97US-0065848P.
 18-NOV-1997; 97US-0065693P.
 21-NOV-1997; 97US-0066120P.
 21-NOV-1997; 97US-0066364P.
 24-NOV-1997; 97US-0066453P.
 24-NOV-1997; 97US-0066466P.
 24-NOV-1997; 97US-0066511P.
 24-NOV-1997; 97US-0066770P.
 24-NOV-1997; 97US-0066772P.
 25-NOV-1997; 97US-0066840P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 PI
 XX
 XX WPI: 1999-229533/19.
 DR N-PSDB; AAX52259.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration.
 XX
 PS Claim 12; Fig 92; 320pp; English.
 XX
 CC AAY13344-403 represent secreted and transmembrane human proteins. The
 CC CDNA sequences are obtained from cDNA libraries, prepared from fetal
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 CC encoded polypeptides have specific uses based on their homology to known
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 CC with the preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
 CC and development, diseases related to growth or survival of nerve cells
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 CC cancer. PRO245 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX
 SQ Sequence 314 AA;
 Query Match 96.4%; Score 1728; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPEQEARPLSGPGRVITSRIVGGEDAEIGRHPWQSLR 73
 Db 1 MGARGALLALLARAGLRKPEQEARPLSGPGRVITSRIVGGEDAEIGRHPWQSLR 60
 QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDFSGMWVQFQSLTSMPSFSLQAYTRYF 133
 Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDFSGMWVQFQSLTSMPSFSLQAYTRYF 120
 QY 134 VSNLYSPRYLGNRPYDIALVKLSAPVTYTKHIQIPICLOASTFEFENRTDCWVTGWGYYK 193
 Db 121 VSNLYSPRYLGNRPYDIALVKLSAPVTYTKHIQIPICLOASTFEFENRTDCWVTGWGYYK 180
 QY 194 EDEALPSHTLQEQVVALINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 253

Db 181 EDEALPSPHTLQEVQVAIINNSCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFDGSGG 240
 QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 313
 Db 241 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
 QY 314 FFPLLWALPLLGPV 327
 Db 301 FFPLLWALPLLGPV 314

RESULT 6
 AAB12132
 ID AAB12132 standard; protein; 314 AA.
 XX
 AC AAB12132;
 XX
 DT 02-FEB-2001 (first entry)
 DE
 DE Hydrophobic domain protein from clone HP03116 isolated from KB cells.
 XX
 KW Human; secreted protein; membrane protein; hydrophobic domain;
 KW proliferation control; differentiation induction; material transport;
 KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
 KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
 KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO200029448-A2.
 XX
 XX 25-MAY-2000.
 XX
 XX 17-NOV-1999; 99WO-JP006412.
 XX
 XX 17-NOV-1998; 98JP-00326255.
 XX
 XX 22-DEC-1998; 98JP-00364315.
 XX
 XX 16-MAR-1999; 99JP-00069811.
 XX
 XX 27-APR-1999; 99JP-00119299.
 XX
 XX 19-MAY-1999; 99JP-00138169.
 XX
 XX (SAGA) SAGAMI CHEM RES CENT.
 XX
 XX (PROT-) PROTEGENE INC.
 XX
 XX Kato S, Kimura T;
 XX
 XX WPI; 2000-387753/33.
 XX
 XX N-PSDB; AAA62005, AAA62015.
 XX
 XX Proteins comprising hydrophobic regions, such as secretory and membrane
 PT proteins, useful in research and diagnostics and having various
 PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
 PT hemostatic, thrombolytic.
 XX
 XX Claim 1; Page 238-240; 410pp; English.
 XX
 XX Secretory proteins play important roles in the proliferation control, the
 CC differentiation induction, the material transport and the biophylaxis of
 CC cells. Membrane proteins have important roles as signal receptors, ion
 CC channels and transporters. The present sequence is a human protein which
 CC has at least one hydrophobic domain. This protein may be a secretory or a
 CC membrane protein. The present protein may have cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, haematopoiesis activity, tissue growth activity,
 CC activ/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, anti-inflammatory activity and tumour
 CC inhibition activity. The present protein could therefore be used for
 CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
 CC disease, and cancer
 XX
 XX Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 3; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPFESQEAAPLSPGCGRRVITSRIYVGDEAELGRWPQGSRLR 73
 Db 1 MGARGALLALLARAGLRKPFESQEAAPLSPGCGRRVITSRIYVGDEAELGRWPQGSRLR 60
 QY 74 LWDSHVCGVSLLSHRWALTAARCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYTYRYF 133
 Db 61 LWDSHVCGVSLLSHRWALTAARCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYTYRYF 120
 QY 134 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 193
 Db 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 180
 QY 194 EDEALPSPHTLQEVQVAIINNSCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFDGSGG 253
 Db 181 EDEALPSPHTLQEVQVAIINNSCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFDGSGG 240
 QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 313
 Db 241 PLACNKNGLWYQIGVSWGVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
 QY 314 FFPLLWALPLLGPV 327
 Db 301 FFPLLWALPLLGPV 314

RESULT 7
 ADC78569
 ID ADC78569 standard; protein; 314 AA.
 XX
 AC ADC78569;
 XX
 DT 01-JAN-2004 (first entry)
 DE
 DE Human PRO303 protein.
 XX
 KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW antirheumatic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; cardiast; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
 KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 XX diabetes; stroke; gene therapy; transgenic; PRO; human.
 XX
 OS Homo sapiens.
 XX
 XX WO200015796-A2.
 XX
 XX 23-MAR-2000.
 XX
 XX 15-SEP-1999; 99WO-US021090.
 XX
 XX 16-SEP-1998; 98WO-US019330.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 XX Yuan J;
 XX WPI; 2000-271434/23.
 XX N-PSDB; ADC78568.
 XX
 XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX

PS Claim 12; SEQ ID NO 257; 355pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO protein of the invention.
 XX
 SQ Sequence 314 AA;

 Query Match 96.4%; Score 1728; DB 3; Length 314;
 Best Local Similarity 100.0%; Pred. NO. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGDEAELGRWPQGSRLR 73
 DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGDEAELGRWPQGSRLR 60

 QY 74 LWDHVCGVSLLSHRWALTAHCFETYSDSLSDPSGMVQFQGLTSMPSFWSLQAYTRYF 133
 DB 61 LWDHVCGVSLLSHRWALTAHCFETYSDSLSDPSGMVQFQGLTSMPSFWSLQAYTRYF 120

 QY 134 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYIK 193
 DB 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYIK 180

 QY 194 EDEALPSFHTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
 DB 181 EDEALPSFHTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240

 QY 254 PLACNKNGLWYQIGVSWGVCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 313
 DB 241 PLACNKNGLWYQIGVSWGVCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 300

 QY 314 FFPLLWALPLLGPV 327
 DB 301 FFPLLWALPLLGPV 314

 RESULT 8
 AAB80256
 ID AAB80256 standard; protein; 314 AA.
 AC AAB80256;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO303 protein.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antineumatic; cancer;
 KW antiarthritic; antifertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN W0200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000WO-US0004414.
 XX
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR

28-JUL-1999; 99US-0146222P.
 08-SEP-1999; 99WO-US020594.
 13-SEP-1999; 99WO-US020944.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 05-OCT-1999; 99WO-US023089.
 23-NOV-1999; 99WO-US028214.
 30-NOV-1999; 99WO-US028313.
 02-DEC-1999; 99WO-US028564.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 20-DEC-1999; 99WO-US030911.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin LJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 WPI; 2001-081051/09.
 N-PSDB; AAF72417.
 XX
 XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
 PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
 PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
 PT disease).
 XX
 PS Claim 1; Fig 92; 393pp; English.
 XX
 CC The present sequence is one of sixty one novel secreted and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful for treating skin
 CC diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis),
 CC ischaemia such as coronary ischaemia, atherosclerosis), inflammatory
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping
 XX
 SQ Sequence 314 AA;

 Query Match 96.4%; Score 1728; DB 4; Length 314;
 Best Local Similarity 100.0%; Pred. NO. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGDEAELGRWPQGSRLR 73
 DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGDEAELGRWPQGSRLR 60

 QY 74 LWDHVCGVSLLSHRWALTAHCFETYSDSLSDPSGMVQFQGLTSMPSFWSLQAYTRYF 133
 DB 61 LWDHVCGVSLLSHRWALTAHCFETYSDSLSDPSGMVQFQGLTSMPSFWSLQAYTRYF 120

 QY 134 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYIK 193
 DB 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYIK 180

 QY 194 EDEALPSFHTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
 DB 181 EDEALPSFHTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240

 QY 254 PLACNKNGLWYQIGVSWGVCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 313
 DB 241 PLACNKNGLWYQIGVSWGVCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 300

 QY 314 FFPLLWALPLLGPV 327

CC diseases and abnormalities or susceptibility to diseases related to
 CC presence of mutations in the nucleic acid sequences which encode the
 CC enzyme. Pharmaceutical composition comprising esp-1 like enzyme is useful
 CC for treating dermatitis, Paget's disease, and preventing degradation of
 CC bone implants particularly dental implants. The present sequence is human
 CC esp-1 like enzyme
 XX
 XX Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 5; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 MGARGALLALLARAGLRKPESDEAAPLSPGCGRRVITSRVGGEDAEIGRWPMQGLR 73
 DB 1 MGARGALLALLARAGLRKPESDEAAPLSPGCGRRVITSRVGGEDAEIGRWPMQGLR 60
 QY 74 LWDHVGCVSLSHRWALTAACFETYSDDLSDPSGMVQFGLTSMPSFWSLQAYTRYF 133
 DB 61 LWDHVGCVSLSHRWALTAACFETYSDDLSDPSGMVQFGLTSMPSFWSLQAYTRYF 120
 QY 134 VSNIVLSPRYLGNPFDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGIK 193
 DB 121 VSNIVLSPRYLGNPFDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGIK 180
 QY 194 EDEALPSPHTLQEQVVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 253
 DB 181 EDEALPSPHTLQEQVVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
 QY 254 PLACKNGLWQIGVSVGVCGRPNRPVYTNISHFEWIOKLMAQSGMSQDDPSWPLL 313
 DB 241 PLACKNGLWQIGVSVGVCGRPNRPVYTNISHFEWIOKLMAQSGMSQDDPSWPLL 300
 QY 314 FFPLLWALPLIGPV 327
 DB 301 FFPLLWALPLIGPV 314

RESULT 11

ABU71634
 ID ABU71634 standard; protein; 314 AA.

XX AC ABU71634;

XX DT 16-JUN-2003 (first entry)

XX DE Human PRO polypeptide #45.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW pathological disorder; cardiac insufficiency disorder; protein secretion;
 KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
 KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
 KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
 KW cytostatic; cardiac; endocrine; antidiabetic; gastrointestinal;
 KW antiulcer; dermatological; vulnary.

XX OS Homo sapiens.

XX PN US2002146709-A1.

XX PD 10-OCT-2002.

XX PF 18-JUL-2001; 2001US-00909088.

XX PR 17-SEP-1997; 97US-0059113P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 17-SEP-1997; 97US-0059117P.

XX PR 17-SEP-1997; 97US-0059119P.

XX PR 17-SEP-1997; 97US-0059121P.

XX PR 17-SEP-1997; 97US-0059122P.

XX PR 17-SEP-1997; 97US-0059184P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059266P.

PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062818P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030895.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 2000WO-US000219.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PA
 XX

PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-328338/31.
DR N-PSDB; ACA59107.
XX
XX Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX
XX Claim 12; Fig 92; 473pp; English.
XX
CC The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polypeptide of the invention
XX
XX Sequence 314 AA;
SQ

Query Match 96.4%; Score 1728; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLIALLARAGLRKPSQEAAPLSGCGRRVITSRIVGGEDAEIAGRWPGSLR 73
Db 1 MGARGALLIALLARAGLRKPSQEAAPLSGCGRRVITSRIVGGEDAEIAGRWPGSLR 60
QY 74 LWDSHVCGVLSLSHRWALTAACFCFETYSLDSPSGMWVQFGOLTSPSPFWSLQAYYTRYF 133
Db 61 LWDSHVCGVLSLSHRWALTAACFCFETYSLDSPSGMWVQFGOLTSPSPFWSLQAYYTRYF 120
QY 134 VSNIIYLSRYLGNPSYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 193
Db 121 VSNIIYLSRYLGNPSYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 180
QY 194 EDEALPSPTLCEVQVAIIINNSVNCNHLFLKYSFRKDIQDMVCAGNAGGKDACFGDSGG 253
Db 181 EDEALPSPTLCEVQVAIIINNSVNCNHLFLKYSFRKDIQDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVYVSWGVGGRPNRPVYTNISHFEWIKLMAQSGMSQDPSPWPLL 313
Db 241 PLACNKNGLWYQIGVYVSWGVGGRPNRPVYTNISHFEWIKLMAQSGMSQDPSPWPLL 300
QY 314 FPELLWALPLIGPV 327
Db 301 FPELLWALPLIGPV 314

RESULT 12
ABU71489
ID ABU71489 standard; protein; 314 AA.
AC
XX
XX ABU71489;
XX
DT 10-JUN-2003 (first entry)
XX
XX Human PRO polypeptide #45.
DE
XX
XX Human; secreted and transmembrane protein; PRO polypeptide; cancer;
KW Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW

KW neuroprotective.
XX
XX Homo sapiens.
XX
XX US2002192659-A1.
XX
XX 19-DEC-2002.
XX
XX 10-JUL-2001; 2001US-00902853.
XX
XX 17-SEP-1997; 97US-00591113P.
XX 17-SEP-1997; 97US-00591115P.
XX 17-SEP-1997; 97US-00591117P.
XX 17-SEP-1997; 97US-00591119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
XX 28-OCT-1997; 97US-0063550P.
XX 28-OCT-1997; 97US-0063564P.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
XX 18-NOV-1997; 97US-0065693P.
XX 21-NOV-1997; 97US-0066120P.
XX 21-NOV-1997; 97US-0066364P.
XX 24-NOV-1997; 97US-0066453P.
XX 24-NOV-1997; 97US-0066466P.
XX 24-NOV-1997; 97US-0066511P.
XX 24-NOV-1997; 97US-0066772P.
XX 24-NOV-1997; 97US-0066772P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 01-DEC-1998; 98WO-US025108.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 30-MAR-2000; 2000WO-US007377.
 PR 20-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrata N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 XX WPI; 2003-361832/34.
 DR N-PSDB; ACA58504.
 XX
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
 PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 12; Fig 92; 474pp; English.
 XX
 CC The present invention relates to the isolation of novel human secreted
 CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
 CC sequences encoding them. The polynucleotide sequences are useful in
 CC molecular biology, as hybridisation probes, in chromosome and gene
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide sequences may also be used in preparing PRO polypeptides
 CC by recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The PRO polypeptides or
 CC their antibodies are useful in preparing a medicament for treating a
 CC condition responsive to the polypeptide or antibody, such as cancer,
 CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
 CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
 XX
 SQ Sequence 314 AA;
 Query Match 96.4%; Score 1728; DB 6; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148; Indels 0; Gaps 0;
 Matches 314; Conservative 0; Mismatches 0;
 QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDALGRWPQGSRLR 73
 Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDALGRWPQGSRLR 60
 QY 74 LWDSHVCGVSLSHRWALTAHCFETYSYDLSDPSGWMVQFGLTSPSPFSLQAYTRYF 133
 Db 61 LWDSHVCGVSLSHRWALTAHCFETYSYDLSDPSGWMVQFGLTSPSPFSLQAYTRYF 120
 QY 134 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEPENRTDCWVTGWGYIK 193
 Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEPENRTDCWVTGWGYIK 180
 QY 194 EDEALSPHTLOEQVAIINNSCNHLFLKYSFRKDI FGDWVCAGNAQGGKACFGDSGG 253
 Db 181 EDEALSPHTLOEQVAIINNSCNHLFLKYSFRKDI FGDWVCAGNAQGGKACFGDSGG 240
 QY 254 PLACNKNGLWYQIGVSWGCGCRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
 Db 241 PLACNKNGLWYQIGVSWGCGCRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300

QY 314 FPFLWALPLIGPV 327
 Db 301 FPFLWALPLIGPV 314
 RESULT 13
 ABU71935
 ID ABU71935 standard; protein; 314 AA.
 XX
 AC ABU71935;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO303.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; gene therapy;
 KW chromosome identification; chromosome marker.
 XX
 OS Homo sapiens.
 PN US2003003530-A1.
 XX
 PD 02-JAN-2003.
 XX
 PF 11-JUL-2001; 2001US-00904011.
 XX
 PR 17-SEP-1997; 97US-00591113P.
 PR 17-SEP-1997; 97US-00591115P.
 PR 17-SEP-1997; 97US-00591117P.
 PR 17-SEP-1997; 97US-00591119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059132P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059286P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 12-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-00666466P.

PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashtenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D;
 PI Williams PM, Wood WI;
 XX
 WPI: 2003-329602/31.
 DR N-PSDB; ACA60211.
 XX
 PT New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing.
 XX
 PS Claim 12; Fig 92; 484pp; English.
 XX
 CC The invention relates to an isolated nucleic acid with at least 80%
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 CC PRO protein extracellular domain. Also included are a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 CC polypeptide (by culturing the host cell for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),
 CC an isolated PRO polypeptide (having at least 80% sequence identity to:
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 CC number (detailed in the specification); or (c) an extracellular domain of
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 CC peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
 CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
 CC modulating at least one biological activity of a cell expressing a PRO245
 CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
 CC transgenic animals or knock-out animals which may be used in the
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy, in chromosome identification, as
 CC chromosome markers, or in generating probes. The PRO polypeptides are

CC useful as molecular markers for protein electrophoresis, and the isolated
 CC nucleic acids may be used for recombinantly expressing those markers. The
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence represents a PRO protein
 XX
 SQ Sequence 314 AA;
 Query Match 96.4%; Score 1728; DB 6; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.8e-148;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 14 MGARGALLIALILARAGLRKPESQEAAPLSGPCGRRVITSRIYGGDAELGRWPWQSLR 73
 Db 1 MGARGALLIALILARAGLRKPESQEAAPLSGPCGRRVITSRIYGGDAELGRWPWQSLR 60
 Qy 74 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDFSGMWVQGLTSMPSFWSLQAYTRYF 133
 Db 61 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDFSGMWVQGLTSMPSFWSLQAYTRYF 120
 Qy 134 VSNIIYSPRYLGNSPYDIALVLSAPVYTKHQICLOASTPEFENRTDCWVTGWYIK 193
 Db 121 VSNIIYSPRYLGNSPYDIALVLSAPVYTKHQICLOASTPEFENRTDCWVTGWYIK 180
 Qy 194 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSRDKIFGDMVCAGNAQGGKACFGDSGG 253
 Db 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSRDKIFGDMVCAGNAQGGKACFGDSGG 240
 Qy 254 PLACNKNGLWYQIGVSVGWGCGRPNRPVGYTNISSHFEWIKLMAQSGMSQDPSPWPLL 313
 Db 241 PLACNKNGLWYQIGVSVGWGCGRPNRPVGYTNISSHFEWIKLMAQSGMSQDPSPWPLL 300
 Qy 314 FFELLWALPLGPV 327
 Db 301 FFELLWALPLGPV 314
 RESULT 14
 ABO01818
 ID ABO01818 standard; protein; 314 AA.
 XX
 AC ABO01818;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO303.
 XX
 KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; Parkinson's disease;
 KW Alzheimer's disease; inflammation; nephritis; wound healing;
 KW nerve repair; collateral blood vessel formation; cancer;
 KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
 KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
 KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
 KW infertility; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US2002197671-A1.
 XX
 XX 26-DEC-2002.
 XX
 XX 17-JUL-2001; 2001US-00907824.
 PF
 XX 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059119P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.

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PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-DEC-1998; 98WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 20-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX PA
(GETH ) GENENTECH INC.
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XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-370793/35.
DR N-PSDB; ACD07611.
XX
```

New Genes and secreted and transmembrane polypeptides (e.g. PRO245 or PRO335), useful for treating or diagnosing e.g. Alzheimer's disease, cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia or strokes.

Claim 12; Fig 92; 482pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide comprising any of 61 sequences having 164-119 amino acids fully defined in the specification. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. Parkinson's disease, Alzheimer's disease, inflammations, nephritis, wound healing, nerve repair, collateral blood vessel formation, cancers (e.g. colorectal cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs, restenosis, atrophic conditions (e.g. keloids or scarring), ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats, or rabbits). The PRO polypeptides are useful as targets for therapeutic intervention in these diseases, and diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 14 MGARGALLALLARAGLRKPESEAPLSGPCGRVITSRVGGEDALGRWPQGSRLR 73
Db 1 MGARGALLALLARAGLRKPESEAPLSGPCGRVITSRVGGEDALGRWPQGSRLR 60
QY 74 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGMMVQFGLTSMPSLQAYTRYF 133
Db 61 LWDSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGMMVQFGLTSMPSLQAYTRYF 120
QY 134 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEPENRDCWWTGMYIK 193
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEPENRDCWWTGMYIK 180
QY 194 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSPRKDFGDMVCAGNAQGGKACFDGSGG 253
Db 181 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSPRKDFGDMVCAGNAQGGKACFDGSGG 240
QY 254 PLACNKNGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKMLAQSGMSQDPDPNPL 313
Db 241 PLACNKNGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKMLAQSGMSQDPDPNPL 300
QY 314 FFPLLWALPLLGPV 327
Db 301 FFPLLWALPLLGPV 314
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RESULT 15

ABU54391
ID ABU54391 standard; protein; 314 AA.
XX AC ABU54391;
XX DT 10-MAR-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO303.
XX KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
KW Gastrointestinal ulceration; skin disease;
KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; inflammatory disease;
KW rheumatoid arthritis; asthma; multiple sclerosis;
KW atherosclerosis; cardiac injury; infertility; birth defect;
KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
KW diabetic complication; wound repair.
XX OS Homo sapiens.
XX XX
XX PN US2002132240-A1.
XX PD 19-SEP-2002.
XX PF 18-JUL-2001; 2001US-00909320.
XX PR 17-SEP-1997; 97US-00591113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 18-SEP-1997; 97US-0062125P.
PR 18-SEP-1997; 97US-0062285P.
PR 18-SEP-1997; 97US-0062287P.
PR 18-SEP-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063341P.
PR 28-OCT-1997; 97US-0063342P.
PR 28-OCT-1997; 97US-0063344P.
PR 28-OCT-1997; 97US-0063349P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063708P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
XX PA Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Fertara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ,
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
DR WPI; 2003-147434/14.
DR N-PSDB; ABX71659.
XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or
PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
PT disease.
XX Claim 12; Fig 92; 473pp; English.
XX The invention relates to an isolated PRO polypeptide having at least 80%
CC amino acid sequence identity to: (a) any one of 61 fully defined amino
CC acid sequences given in the specification (appearing as ABU54347-
CC ABU54407); (b) an amino acid sequence encoded by the nucleotide sequence
CC deposited under American Type Culture Collection (accession numbers
CC listed in the specification); (c) any one of the PRO sequences which
CC lacks its associated signal peptide; (d) an extracellular domain of the
CC PRO polypeptide with its associated signal peptide; or (e) an
CC extracellular domain of the PRO polypeptide which lacks its associated
CC signal peptide. Also include are the nucleic acids encoding the PRO
CC polypeptides, vectors, host cells and anti-PRO antibodies. The PRO
CC polypeptides and nucleic acids are useful in diagnosing or treating
CC enterocolitis, gastrointestinal ulceration, skin diseases associated with
CC abnormal keratinocyte differentiation, e.g. psoriasis or epithelial
CC cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.
CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,
CC atherosclerosis, cardiac injury, infertility, birth defects, premature
CC aging, AIDS, cancer, diabetic complications, or mutations in general. The
CC polypeptides are also useful for wound repair and associated therapies
CC concerned with re-growth of tissue. The nucleotide sequences may be used

CC as hybridisation probes in chromosome and gene mapping, or in generating
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
CC polypeptides, in assays to identify other proteins or molecules involved
CC in binding reaction, to generate transgenic animals or knockout animals,
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, for chromosome identification, and
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies may be used in
CC diagnostic assays for PRO, or for the affinity purification of PRO from
CC recombinant cell culture or natural sources. The present sequence
CC represents a PRO polypeptide
XX
SQ Sequence 314 AA;

Query Match 96.4%; Score 1728; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 5.8e-148;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MCARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGEDAELGRWPQGSRLR 73
DB 1 MCARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGEDAELGRWPQGSRLR 60
QY 74 LWDHVCGVSLLSHRWALTAACFETYSDSLSDPSGMMVQFQOLTSMPFSWLSQAYTRYF 133
DB 61 LWDHVCGVSLLSHRWALTAACFETYSDSLSDPSGMMVQFQOLTSMPFSWLSQAYTRYF 120
QY 134 VSNIVLSPRYLGNSPYDIALVKLSAPVYTYTHIQICLQASTFEFENRTDCWVTGMYIK 193
DB 121 VSNIVLSPRYLGNSPYDIALVKLSAPVYTYTHIQICLQASTFEFENRTDCWVTGMYIK 180
QY 194 EDEALPSPTLQEVQVAIINNMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSPTLQEVQVAIINNMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKGMLWYQIGVSVGCGRENRPQVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 313
DB 241 PLACNKGMLWYQIGVSVGCGRENRPQVYTNISHHFEWIKLMAQSGMSQDPDPSPWPLL 300
QY 314 FPPLLWALPLGPV 327
DB 301 FPPLLWALPLGPV 314

Search completed: April 6, 2004, 14:11:37
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2004, 14:09:59 ; Search time 20 Seconds
(without alignments)
1572.731 Million cell updates/sec

Title: US-09-787-844-2
Perfect score: 1792
Sequence: 1 RQGRGQAGEAMGARGAL.....PSWPLLPFLMLWLPILGPV 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	580	32.4	343	1 A57014	proctasin (EC 3.4.21.1) precursor - human
2	528.5	29.5	270	2 S56160	mast cell tryptase
3	518	28.9	275	2 C35863	tryptase (EC 3.4.21.1)
4	515	28.7	275	2 A35863	tryptase (EC 3.4.21.1)
5	514.5	28.7	275	2 A35863	tryptase (EC 3.4.21.1)
6	514	28.7	275	2 B35863	tryptase (EC 3.4.21.1)
7	513	28.6	275	2 A35863	tryptase (EC 3.4.21.1)
8	512	28.6	275	2 A35863	tryptase (EC 3.4.21.1)
9	511	28.5	275	2 A35863	tryptase (EC 3.4.21.1)
10	511	28.5	275	2 A35863	tryptase (EC 3.4.21.1)
11	507	28.3	273	2 A47246	tryptase (EC 3.4.21.1)
12	503.5	28.1	273	2 A47246	tryptase (EC 3.4.21.1)
13	500	27.9	274	2 JCI171	tryptase (EC 3.4.21.1)
14	483.5	27.0	625	1 KFHU1	coagulation factor
15	477.5	26.6	417	1 S00845	hepsin (EC 3.4.21.1)
16	475.5	26.5	366	2 JE0105	testicular serine
17	456.5	25.5	237	2 S68702	tryptase (EC 3.4.21.1)
18	455.5	25.4	415	1 A34170	tryptase (EC 3.4.21.1)
19	455.5	25.4	810	1 PLHU	acrosin (EC 3.4.21.1)
20	454	25.3	455	2 A61545	plasmin (EC 3.4.21.1)
21	452.5	25.3	436	2 JX0172	acrosin (EC 3.4.21.1)
22	449	25.1	555	2 JC7731	membrane-bound arg
23	448.5	25.0	367	2 JE0104	testicular serine
24	447	24.9	416	1 S33777	hepsin (EC 3.4.21.1)
25	446.5	24.9	421	2 S25699	acrosin (EC 3.4.21.1)
26	446	24.9	1035	1 A40300	enteropeptidase (E
27	444.5	24.8	4548	1 S00657	apoptosein(a)
28	444	24.8	1113	2 JE0315	low-density lipopr
29	443	24.7	1019	1 A56318	enteropeptidase (E

30	439.5	24.5	418	2 A37344	acrosin (EC 3.4.21.1)
31	437.5	24.4	460	2 B61545	plasmin (EC 3.4.21.1)
32	436	24.3	810	2 B30848	plasmin (EC 3.4.21.1)
33	435.5	24.3	431	2 S47538	acrosin (EC 3.4.21.1)
34	435.5	24.3	790	1 PLFG	plasmin (EC 3.4.21.1)
35	435.5	24.3	812	1 PLMS	plasmin (EC 3.4.21.1)
36	433	24.2	812	1 PLBO	plasmin (EC 3.4.21.1)
37	430.5	24.0	437	2 S18407	acrosin (EC 3.4.21.1)
38	430	24.0	421	1 S11674	acrosin (EC 3.4.21.1)
39	430	24.0	786	1 A47547	acrosin (EC 3.4.21.1)
40	428.5	23.9	266	2 S54146	serine proteinase
41	428	23.9	810	2 A46260	trypsin (EC 3.4.21.1)
42	427	23.8	1420	2 A32869	apolipoprotein(a)
43	422	23.5	1524	2 T30337	polyprotein - Afri
44	417	23.3	1034	1 A53663	enteropeptidase (E
45	414	23.1	269	2 B32410	mastocytoma protei

ALIGNMENTS

RESULT 1
A57014
proctasin (EC 3.4.21.1) precursor - human
C:Species: Homo sapiens (man)
C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
C:Accession: A57014; A54866
R:Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A>Title: Molecular cloning, tissue-specific expression, and cellular localization of hu
A:Reference number: A57014; MUID:95286644; PMID:7768952
A:Accession: A57014
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-343 <RES>
A:Cross-references: GB:L41351; NID:G862304; PIDN:AAC41759.1; PID:G862305
A:Experimental source: prostate
A>Note: parts of this sequence were determined by protein sequencing
R:Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A>Title: Proctasin is a novel human serine proteinase from seminal fluid. Purification,
A:Reference number: A54866; MUID:94308140; PMID:8034638
A:Accession: A54866
A:Molecule type: protein
A:Residues: 45-64 <YUA>
C:Genetics:
C:Gene: GDB:PRSS8
A:Cross-references: GDB:676446; OMIM:600823
A:Map position: 16p11.2-16p11.2
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-44/Domain: signal sequence #status predicted <MAT>
F:33-44/Domain: product: proctasin #status predicted <CHL>
F:45-343/Domain: proctasin light chain #status predicted <CHL>
F:45-281/Domain: trypsin heavy chain #status predicted <CHH>
F:323-341/Domain: trypsin homology <TRY>
F:323-341/Domain: transmembrane #status predicted <TM1>
F:37-154,70-86,168-244,201-223,234-262/disulfide bonds: #status predicted
F:85,134,238/Active site: His, Asp, Ser #status predicted
F:159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 32.4%; Score 580; DB 1; Length 343;
Best Local Similarity 40.6%; Pred. No. 3.7e-44;
Matches 146; Conservative 47; Mismatches 107; Indels 60; Gaps 14;

Qy	3	QKGVLPFGQ--LGA-VAILLYGLLRSG-TGAGGAA-----PCG-VAQARTTGSSAV 62
Db	3	QKGVLPFGQ--LGA-VAILLYGLLRSG-TGAGGAA-----PCG-VAQARTTGSSAV 52
Qy	63	LGRWPWGSLRLWDSHVGCVSLSHRWALTAHCFETYSDLSDPS-----GMMVQFG--Q 115
Db	53	AGQWPQWQSVITBEGHVGCVSLSEQWLSAAHCF-----PSBHKEAYEVKLGAHQ 104

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QY 116 LTSMPSPWSLOAYTVRFVFNINYLSPRYL-GNSPYDIALVKLSAPVYTKHIQPICLQAS 174
Db 105 LDS-----YSEDAKYST--LKDIIIPHSYLOEGSGDIALQLSRPITFRSYRIPICLPAA 158
QY 175 TFEENRTDCWVTGWTGVIKEDALPSHTLOEQVVAIINSMCNHLF---LKYSRPRKDF 231
Db 159 NASFPNGLHCTVTGHWGVAHSVSLTTPKPLQQLVPLISRETNCNLYNIDAKBEEBHFVQ 218
QY 232 GDMVCAGNAQGGKDACFGDSGGPLACNKGWLTQIGVWSGVGCGRPNRPVGVYTNISHHF 291
Db 219 EDMVCAGYVEGGKDACGDSGGPLSCPVEGLWLTGIVSGDAGCAGRNRPVGVYTLASSYA 278
QY 292 EWIO-----KLMAQSGWSQDDPSW-----PILFPELLWALPLIGP 326
Db 279 SWIQSKVTELOPRVVPQTQESQPSNLCGSHLAFSSAPAGQLRPLFLPLGLAUGLLSP 338

RESULT 2
S56160
mst cell tryptase precursor - Mongolian jird
C:Species: Meriones unguiculatus (Mongolian jird)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C:Accession: S56160
R:Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N
Biochem. J. 309, 921-926, 1995
A:Title: Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil, Meriones
A:Reference number: S56160; MUID:95366971; PMID:7639711
A:Accession: S56160
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <MUR>
A:Cross-references: EMBL:D31789; NID:G517122; PIDN:BAA06598.1; PID:G517123
C:Superfamily: trypsin; trypsin homology
F:26-262/Domain: trypsin homology <TRY>

Query Match 29.5%; Score 528.5; DB 2; Length 270;
Best Local Similarity 40.5%; Pred. No. 1.1e-39;
Matches 118; Conservative 36; Mismatches 92; Indels 45; Gaps 9;

QY 20 LLLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGDAELGRWPQGSLSR---LW 75
Db 5 LLLALPLFLMHRSPLCQEWG-----IVGQEAEPGNKWPQVSLRANETYW 50
QY 76 DSHVCGVSLLSHRWALTAHCFTYSLSDPSPGWMVQFGQLTSMPSFWSLQAYTRYF-- 133
Db 51 -RHFCGSLIHPQWLTAHC--VGPTIADPNKVRVQ-----LRKQLYYHDE 95
QY 134 ---YSNTLYLSPR-YLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGW 189
Db 96 LLAVSRITHTFTFATQNGADIALLELKNPNVSSHVPVSLPPASSETFPGTLCWVTGW 155
QY 190 GYIKEDALPSHTLOEQVVAIINSMCNHLFLKYSFRKD-----IFGDMVCAGNAQGGKD 245
Db 156 GNINDVSLPPPPFLPKVQVVENQLCDLKHKGVTGTGNIIHVRDDMLCAGNE--GHD 213
QY 246 ACFGDSGGPLACNKGWLTQIGVWSGVGCGRPNRPVGVYTNISHHFETIQX 296
Db 214 SCQDGGPLVCKVNGTWLQAGVWSWEGCALPNRPGIYTRVYYLDWIHR 264

RESULT 3
C35863
tryptase (EC 3.4.21.59) III precursor - human
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Mar-2003
C:Accession: C35863; E35863; A38893
R:Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
A:Reference number: C35863; MUID:90251647; PMID:2187193
A:Accession: C35863
A:Molecule type: mRNA
A:Residues: 9-275 <VAN>

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A:Accession: E35863
A:Molecule type: DNA
A:Residues: 1-9 <VA2>
A:Cross-references: GB:M33494; NID:G3927804; PIDN:AAC83172.1; PID:G339977
A>Note: the first nine residues of this sequence are inferred from genomic DNA of trypt
R:Vanderslice, P.
Submitted to GenBank, April 1990
A:Reference number: A38893
A:Accession: A38893
A:Molecule type: mRNA
A:Residues: 9-131, 'K', 132-275 <VA3>
A:Cross-references: GB:M33493; NID:G339984; PIDN:AAA36780.1; PID:G339985
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:22-30/Domain: signal sequence #status predicted <SIG>
F:31-275/Product: activation peptide #status predicted <ACT>
F:31-267/Domain: trypsin homology <TRY>
F:74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 28.9%; Score 518; DB 2; Length 275;
Best Local Similarity 40.4%; Pred. No. 1e-38;
Matches 116; Conservative 42; Mismatches 93; Indels 36; Gaps 10;

QY 20 LLLAL--LLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGDAELGRWPQGSLSRWD- 76
Db 5 LLLALPVLASRA-----YAAPAQALQV---GIVGQEAAPRSKWPQVSLVRDR 53
QY 77 --SHVCGVSLLSHRWALTAHCFTYSLSDPSPGWMVQFGQLTSMPSFWSLQAYTRYF- 133
Db 54 YMHFCGSLIHPQWLTAHC--VGPDVKDLAALRVQLRE-----OHLYYQDOLL 102
QY 134 -VSNITLYLSPR-YLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGW 191
Db 103 PVSRIIVHPQYTAQIGADIALLELPEPVNVSSHVPVSLPPASSETFPGCPWVTGWGD 162
QY 192 IKEDEALPSHTLOEQVVAIINSMCNHLFLKYSFRKD-----IFGDMVCAGNAQGGKDAC 247
Db 163 VNDERLPPPPFLPKVQVVENQLCDLKHKGVTGTGNIIHVRDDMLCAGNTR--RDSC 220
QY 248 FGDSGGPLACNKGWLTQIGVWSGVGCGRPNRPVGVYTNISHHFEWI 294
Db 221 QDGGGPLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYYLDWI 267

RESULT 4
A35863
tryptase (EC 3.4.21.59) I precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C:Accession: A35863; D35863; A60939; A39326
R:Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine f
A:Reference number: A35863; MUID:90251647; PMID:2187193
A:Accession: A35863
A:Molecule type: DNA
A:Residues: 1-275 <VAN>
A:Cross-references: GB:M33494; NID:G3927804; PIDN:AAC83172.1; PID:G339977
A:Accession: D35863
A:Molecule type: mRNA
A:Residues: 1-275 <VA2>
A:Cross-references: GB:M33491
R:Butterfield, J.H.; Weller, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C.
J. Leukoc. Biol. 47, 409-419, 1990
A:Title: Purification of tryptase from a human mast cell line.
A:Reference number: A60939; MUID:90244210; PMID:2110591
A:Accession: A60939
A:Molecule type: protein
A:Residues: 31-38, 'P', 40-41, 'X', 43, 'T', 45-48, 'X', 50 <BUT>
A:Experimental source: mast cell
A>Note: 44-Gly was also found
R:Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chretien

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J. Biol. Chem. 262, 1363-1373, 1987
A;Title: Human pituitary trypsin: molecular forms, NH-2-terminal sequence, immunocytoch
A;Reference number: A39326; MUID:87109258; PMID:3543004
A;Accession: A39326
A;Molecule type: protein
A;Residues: 31-38 <CRO>
A;Experimental source: pituitary
C;Genetics:
A;Introns: 21/1; 78/2; 177/1; 221/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: trypsin I #status experimental <NAI>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 28.7%; Score 515; DB 2; Length 275;
Best Local Similarity 40.3%; Pred. No. 1.9e-38;
Matches 116; Conservative 42; Mismatches 92; Indels 38; Gaps 11;
QY 20 LLLAL--LLARAGLRKPSQEAAPISGCGRRVITSIRVIGGEDAELGRWPQGSRL--- 74
DB 5 LLLALPVLASRA-----YAAPAGQALQRV---GIVGGQAPRSKWPQVSLRVHGP 53
QY 75 -NDSHVCVSLSHRWALTAACHCFETYSDLSPSCMWVQFQLTSMPSFWSLQAYTRYF 133
DB 54 YR-MHFCGSLHPQWLTIAHC--VGPDVKDLAALRVQLRE-----CHLYYQDL 101
QY 134 --VSNIIYSPR-YLGNSPYDIALVKSAPVTVTKHIQICLQASTFEFENRTDCWVTGW 190
DB 102 LPVSRIIVHFPQYTAIGADIALLEBPVNVSSHVHTVTPPASETTPPGMPCWVTGW 161
QY 191 YKEDALPSPHTLQEVQVAIINNSMCHLFLKYSFRD----TPGDMVCAGNAGQGD 246
DB 162 DVDNDRUPPPPLKQVQKPVIMENHICDAKHLGATGDDVRIVRDDMLCAGNTR--RDS 219
QY 247 CFGDSGGPLACNKLWQIGVSVGVGGRNRRGVNTNISHPEWI 294
DB 220 CQDGGGFLVCKVNTWLAGVSVGEGCAQNPRIYTRYIYLDWI 267

RESULT 5
KQMSPL
A;Title: Mouse plasma kallikrein (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A36557
R;Seidah, N.G.; Sawyer, N.; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont
DNA Cell Biol. 9, 737-748, 1990
A;Title: Mouse plasma kallikrein: cDNA structure, enzyme characterization, and compariso
A;Reference number: A36557; MUID:91090844; PMID:2264928
A;Molecule type: mRNA
A;Accession: A36557
A;Residues: 1-638 <SEI>
A;Cross-references: GB:M59588; NID:g200358; PIDN:AAA63393.1; PID:g200359
A;Note: part of this sequence, including the amino ends of both the heavy and light cha
C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
are linked by one or more disulfide bonds.
C;Superfamily: coagulation factor XI; trypsin homology
C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-390/Product: plasma kallikrein heavy chain #status experimental <HCH>
F;20-109/Domain: apple repeat <AP1>
F;110-199/Domain: apple repeat <AP2>
F;200-289/Domain: apple repeat <AP3>
F;291-380/Domain: apple repeat <AP4>
F;391-638/Product: plasma kallikrein light chain #status experimental <LCH>
F;391-621/Domain: trypsin homology <TRY>
F;21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,318-347,322
F;127,215,308,396,494/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;434,483,578/Active site: His, Asp, Ser #status predicted

Query Match 28.7%; Score 514.5; DB 1; Length 638;
Best Local Similarity 40.2%; Pred. No. 5.8e-38;
Matches 101; Conservative 43; Mismatches 84; Indels 23; Gaps 8;
QY 51 ITSRIIVGDEDAELGRWPQGSRL---LWDSHVCVSLSHRWALTAACHCFE--TYSDLS 105
DB 387 INARIIVGGTNASLGEWFPQVSLQVLSQTHLCGSGIIGRWYLTAAHCFDGIPIPDV 446
QY 106 PSGMWVQFGOLT-SMPSFWSLQAYTRYFVSNIIYLSPRY-LGNSPYDIALVKSAPV 163
DB 447 IYGGILSLSEITKETS-----SR--IKELIIHQEYKVSSEGYDIALIKLQTLN 496
QY 164 KHQPICLQASTFEFENRTDCWVTGNGYIKEDALPSPHTLQEVQVAIINNSMCHLFL 223
DB 497 EFQKPICLPSKADTIYTNWVTGNGYTKEQG--ETQNILOKATIFLVNESCCQKYR 554
QY 224 YSPRKDIFGDMVCAGNAGQGDACFGDSGGPLVCKHGRWQLVGIISWEGCGRKDP 283
DB 555 YVINK-----QMICAGYKEGGTDACKSDSGGFLVCKHGRWQLVGIISWEGCGRKDP 610
QY 284 YTNISHFEWI 294
DB 611 YTKVSYMDWI 621

RESULT 6
B35863
A;Title: Human mast cell trypsin: multiple cDNAs and genes reveal a multigene serine p
A;Reference number: A35863; MUID:90251647; PMID:2187193
A;Accession: B35863
A;Molecule type: mRNA; DNA
A;Residues: 1-275 <VAN>
A;Cross-references: GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983
A;Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic
R;Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Clin. Invest. 86, 864-870, 1990
A;Title: Cloning and characterization of a second complementary DNA for human trypsin.
A;Reference number: A37193; MUID:90369005; PMID:2203827
A;Accession: A37193
A;Molecule type: mRNA
A;Residues: 1-275 <MIL>
A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584
R;Blom, T.; Hellman, L.
Scand. J. Immunol. 37, 203-208, 1993
A;Title: Characterization of a trypsin mRNA expressed in the human basophil cell line
A;Reference number: I59473; MUID:93166209; PMID:8434231
A;Accession: I59473
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-275 <RES>
A;Cross-references: GB:S5551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A;Experimental source: basophil cell line KU812
C;Genetics:
A;Gene: GDB:TPS1
A;Cross-references: GDB:125890; OMIM:191080
A;Map position: 16pter-16qter
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: trypsin I #status predicted <NAI>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 28.7%; Score 514; DB 2; Length 275;

Best Local Similarity 40.3%; Pred. No. 2.3e-38;
Matches 116; Conservative 42; Mismatches 92; Indels 38; Gaps 11;
QY 20 LLAL--LLARAGLRKPESQEAAPLSPGCGRRVITTSIVGGEDAEILGRWPQGSRL-- 74
DB 5 LLLALPVLASFA-----YAPAPQALQRV---GIVGQAPSKPWPQVSLVHGP 53
QY 75 -WDSHVGCVSLLSHRWALTAHCFETYSDLSDFSGMMVQFGQUTSMPSFSLQAYTRYF 133
DB 54 YW-MHFCGGSLIHPQWLTAAHC--VGPDKDLAALRVQLRE-----QHLYYQDQL 101
QY 134 --VSNIVLSR-YLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEENRTDCWTGNG 190
DB 102 LPVSRIVHQFYTAQIGALIALLEELPVPKVSHTVTLPPASETFPPGMPFCWTGNG 161
QY 191 YIKEDALPSPHTLQEOVVAIINNSMCNHLFLKYSPK-----IFGDMVCAGNAQGDKA 246
DB 162 DVDNDERLPPFLPKQVKVPMENHICDAKYHLGAYTGDDVIRVDDMLCAGNTR--RDS 219
QY 247 CFCDGSGPLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWI 294
DB 220 CQSDSGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYLDWI 267

RESULT 7
KOHUP
Plasma kallikrein (EC 3.4.21.34) precursor - human
N/Alternate names: kininogenin; plasma prekallikrein
C/Species: Homo sapiens (man)
C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C/Accession: A00921; A37939
R/Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A/Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four
A/Reference number: A00921; MUID:86243359; PMID:3521732
A/Accession: A00921
A/Molecule type: mRNA
A/Residues: 1-638 <CHU>
A/Cross-references: GB:ML3143; NID:G190262; PIDN:AAA60153.1; PID:GI90263
R/McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A/Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
A/Reference number: A37939; MUID:91152016; PMID:1998666
A/Accession: A37939
A/Molecule type: protein
A/Residues: 20-27,40-46,'X',48,'H',50,'X',52-70,'H',75-76,'X',78-80,103-113,131-140,141-
1260,283,'X',285-287,291,'X',293-295,314-317,'X',319-320,321-324,'X',329-333,334-339,'X',
525,538-551,562,'X',564-567,573,'X',575-576,578-583,'X',585,592-604 <MCM>
C/Comment: This protein, synthesized in the liver, circulates as a noncovalent complex
are linked by one or more disulfide bonds.
C/Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a li
inogen and may also play a role in the renin-angiotensin system by converting prorenin i
C/Genetics:
A/Gene: GDB:KLK3
A/Cross-references: GDB:127575; OMIM:229000
A/Map position: 4q35-4q35
C/Superfamily: coagulation factor XI; trypsin homology
C/Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-638/Product: plasma kallikrein #status predicted <MAT>
F:20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F:20-103/Domain: apple repeat <AP1>
F:110-199/Domain: apple repeat <AP2>
F:200-289/Domain: apple repeat <AP3>
F:291-380/Domain: apple repeat <AP4>
F:331-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F:391-621/Domain: trypsin homology <TRY>
F:21-104,47-77,51-57,111-194,137-166,141-147,201-284,227-256,231-237,292-375,322-328,383
F:127,308,396,453,494/Binding site: carboxydrase (Asn) (covalent) #status experimental
F:138-347,340-345/Disulfide bonds: #status predicted
F:390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F:434,483,578/Active site: His, Asp, Ser #status predicted

Query Match 28.6%; Score 513; DB 1; Length 638;
Best Local Similarity 37.5%; Pred. No. 7.8e-38;
Matches 114; Conservative 45; Mismatches 103; Indels 42; Gaps 11;
QY 13 AMGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITTSIVGGEDAEILGRWPQGSRL 72
DB 361 AYTGGSSGYSLRLCNTG-----DNSVCTTKTST-RIVGGTNSNGEWPQVSL 408
QY 73 RL--WDSHVGCVSLLSHRWALTAHCFETYSDLSDFSGMMVQFG-----OLTSMPSPWS 124
DB 409 QVKLTAQRHLGGSLIGHQWLTAAHCFD---GLPLQDVWRIYSGILNLSLITKDTFSG 465
QY 125 LQ--AYTRYFVSNIVLSRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEENRT 182
DB 466 IKEIIHONYKVS-----GN--HDIALIKLQAPLNYTEFOKPICLPSKGTSTIYT 515
QY 183 DOWTGWYIKEDALPSPHTLQEOVVAIINNSMCNHLFLKYSPKDFGDMVCAGNAQ 242
DB 516 NCWTGNGFSKEKEI--QNILQKNIPLVNTECCQRYQDYK-----ITQRMVCAGYKEG 569
QY 243 GKDACFGDSGGPLACNKNGLWYQIGVSWGVCGRPNRPVYTNISHHFEWI-OKLMAQS 301
DB 570 GKDACGDSGGPLVCKHNGMWRLVGITSWGEGCARREQPGVYTKVAEYMDWILEKTOSSD 629
QY 302 GMSQ 305
DB 630 GRAQ 633

RESULT 8
A38654
Mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
C/Accession: A38654; B38654; D35646; I59478
R/Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991
A/Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by
A/Reference number: A38654; MUID:91139682; PMID:1995638
A/Accession: A38654
A/Molecule type: DNA
A/Residues: 1-276 <REY>
A/Cross-references: GB:M57625; NID:G200506; PIDN:AAA39987.1; PID:G200507
s Gly. GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A/Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37
A/Accession: B38654
A/Molecule type: mRNA
A/Residues: 1-276 <RE2>
A/Cross-references: GB:M57626; NID:G200508; PIDN:AAA39988.1; PID:G200509
R/Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A/Title: Different mouse mast cell populations express various combinations of at least
A/Reference number: A35646; MUID:90222202; PMID:2326280
A/Accession: D35646
A/Molecule type: protein
A/Residues: 32-54 <RE3>
R/Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskog, M.; Larsson, L.G.; Nilsson,
Scand. J. Immunol. 38, 359-367, 1993
A/Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
A/Reference number: I59478; MUID:94023807; PMID:8210998
A/Accession: I59478
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-276 <RES>
A/Cross-references: GB:L31853; NID:G473480; PIDN:AAA39725.1; PID:G473481
C/Genetics:
A/Gene: MIM:6
A/Introns: 24/1; 79/2; 168/1; 222/3
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-31/Domain: activation peptide #status predicted <ACT>


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QY 99 -TYSLSLSPSGMVGQGLTSMPSFWSLQAYTRYFVSNIVLSRY-ILGNSPYDIALVKL 156
Db 439 IPYDPVWRIYGGILNLSITNKTFSS-----IKELIHHQYKMSSEGSYDIALIKL 489
QY 157 SAPVTYTKHIQIPICLQAGTFFENRTDCWVTGWGVIKEDALPSPHTLQEVQVAILNNSM 216
Db 490 QTFPLNTYFFQKICLPSKADNTIYTNVNTGWGTYKERG--ETQNILOKATILPVNEE 547
QY 217 CNHLEKYSFRKDIPEGWVVCAGNAGGKDAFCGDSGGPLACNKGKGLWYQIGVSWGVCQG 276
Db 548 CQKYRDYVITK---QMICAGYKEGGIDACKGDSGGPLVCKGSRQWLGVITSGWGGCA 603
QY 277 RPNRPGVYTNISHPHWIQLKMAQS 301
Db 604 RKEQGVYTKVAEYIDWLEIKIQQS 628

RESULT 11
A47246
tryptase (EC 3.4.21.59) 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A47246
R:McNeill, H.P.; Reynolds, D.S.; Schiller, V.; Gildyal, N.; Gurley, D.S.; Austen, K.F.;
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A:Title: Isolation, characterization, and transcription of the gene encoding mouse mast
A:Reference number: A47246; MUID:93087489; PMID:1454796
A:Accession: A47246
A>Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-273 <MCN>
A:Cross-references: GB:L00653; NID:g200518; PID:AAA39992.1; PID:g200519
A>Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBI:P:119746)
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:29-265/Domain: trypsin homology <TRY>

Query Match 28.3%; Score 507; DB 2; Length 273;
Best Local Similarity 42.4%; Pred. No. 9.6e-38;
Matches 114; Conservative 34; Mismatches 87; Indels 34; Gaps 9;

QY 39 AAPLSGCGRRVITSRIYVGGDEALGRWPWGSLRLWDS---HVCVGLLSHRWALTAH 95
Db 18 AAP--GPANTR---EGIVGGQEAHGNKWPQVSLURANDTYMWHFCGSLTHPQWVLTAAH 72
QY 96 CFETYSLSPSGMVGQGLTSMPSFWSLQAYTRYF-----VSNIVLSR-ILGNSPY 149
Db 73 C--VGPDVADENKVRVQ-----LRKQLYYHDLMTVSQIITHPDFVIYQDGA 118
QY 150 DIALVKLSAPTYTKHIQIPICLQASTFEFENRTDCWVTGWGVIKEDALPSPHTLQEVQV 209
Db 119 DIALKLTNPVNI SDYHFVFLPFPASETFPSGTLCTWGTGMDNGVNLNPPFPFLKEVQV 178
QY 210 AIINNSMCHLFLKYSPRKD---IFGDMVCAGNAQGGKDAFCGDSGGPLACNKGKGLWYQ 265
Db 179 PIENHLCDLYKHKLITGDNVHIVRDDMLCAGNE--GHUSCGDSGGPLVCKVEDTWLQ 236
QY 266 IGWVSWGCGCRPNRPNGVYTNISHHFEWI 294
Db 237 AGVSWGSGGCAQPNRPNGVYTRYVTVYLDWI 265

RESULT 12
A45754
tryptase (EC 3.4.21.59) alpha precursor - human
C:Species: Homo sapiens (man)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
C:Accession: A45754; B37193
R:Miller, J.S.; Westin, E.H.; Schwartz, L.B.
J. Clin. Invest. 84, 1188-1195, 1989
A:Title: Cloning and characterization of complementary DNA for human tryptase.
A:Reference number: A45754; MUID:90009311; PMID:2677049
A:Accession: A45754

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A:Molecule type: mRNA
A:Residues: 1-274 <MIL>
A:Cross-references: GB:M30038
R:Miller, J.S.; Moxley, G.; Schwartz, L.B.
J. Miller, Invest. 86, 864-870, 1990
A:Title: Cloning and characterization of a second complementary DNA for human tryptase.
A:Reference number: A37193; MUID:90369005; PMID:2203827
A:Accession: B37193
A:Molecule type: mRNA
A:Residues: 1-274 <MI2>
A:Cross-references: GB:M30038
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-P;
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-274/Product: trypsin I #status predicted <MAT>
F:31-266/Domain: trypsin homology <TRY>
F:74,120,223/Active site: His, Asp, Ser #status predicted

Query Match 28.1%; Score 503.5; DB 2; Length 274;
Best Local Similarity 39.2%; Pred. No. 2e-37;
Matches 112; Conservative 43; Mismatches 96; Indels 35; Gaps 9;

QY 20 LLLAL-LLARAGLRKPESQEARAPLSGPCGRRVITSRIYVGGDEALGRWPWGSLRLWD-- 76
Db 5 LLLALPVLASRAYAAPVQALQQAG-----IVGGQEARPKRPWQVLSLRDRY 54
QY 77 -SHVCGVLSLSHRWALTAHCFETYSDLSDFSGMVGQGLTSMPSFWSLQAYTRYF-- 133
Db 55 WMHFQGGSLTHPQWVLTAAHCLG--PDVKDLATLRLVNSG-----THLYYQDQLLP 102
QY 134 VSNIVLSR-ILGNSPYDIALVKLSAPTYTKHIQIPICLQASTFEFENRTDCWVTGWGVI 192
Db 103 VSRIMVHPQFYITQIGADIALLEEPVNISSRVHTVMDLPASETFPGMPCWVTGWGDV 162
QY 193 KEDALPSPHTLQEVQVAIINNSMCHLFLKYSPRKD---IFGDMVCAGNAQGGKDAFC 248
Db 163 DNDEPLPFPPLKQVKVPMENHICDAKYHLGAYTGDDVRIIRDDMLCAGNSQ--RDSCK 220
QY 249 GDSGGPLACNKGKGLWYQIGVSWGCGCRPNRPNGVYTNISHHFEWI 294
Db 221 GDSGGPLVCKVNGTWLQAGVSWDSEGCQPNRPNGVYTRYVTVYLDWI 266

RESULT 13
JC4171
tryptase (EC 3.4.21.59) precursor - rat
N:Alternate names: mast cell tryptase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C:Accession: JC4171
R:Ide, H.; Itoh, H.; Tcmitta, M.; Murakumo, Y.; Kobayashi, T.; Matuyama, H.; Oeada, Y.;
J. Biochem. 118, 210-215, 1995
A:Title: cDNA sequencing and expression of rat mast cell tryptase.
A:Reference number: JC4171; MUID:96015171; PMID:8537314
A:Accession: JC4171
A:Molecule type: mRNA
A:Residues: 1-274 <IDE>
A:Cross-references: DDBJ:D38455; NID:g556555; PIDN:BAA07486.1; PID:g556556
C:Comment: This enzyme is basically specific for a connective tissue mast cell, it is a
enzyme inhibitors.
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-29/Domain: activation peptide #status predicted <ACT>
F:30-274/Product: mast cell tryptase #status predicted <MAT>
F:30-266/Domain: trypsin homology <TRY>
F:73,120,223/Active site: His, Asp, Ser #status predicted
F:131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.9%; Score 500; DB 2; Length 274;
Best Local Similarity 39.3%; Pred. No. 4.1e-37;

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Matches 116; Conservative 39; Mismatches 102; Indels 38; Gaps 11;

QY 20 LLLALLRAGLRKPESEAPLSPGCGRRVITRIVGDEAELGRWFWQGSRL-----LW 75
 Db 2 LKLLLLLLLSP--ASLVHAAAPC--PVQRV---GIVGREAESKFWQVSLRKFESFW 54
 QY 76 DSHVCGVLLSHRWALTAHCFEYSYDLSDSGVMWQFGQLTSPFSWLSQAYTRY--- 132
 Db 55 -MHFCGGLIHFWQVLTAAHCVGLH--IKSPFLRVQ-----UREQVLYYADQ 99
 QY 133 --FVSNILSPRYLG-NSFYDIALVKLSAPVYTKHQPIQLQASTFEFENRTDCWYTG 189
 Db 100 LLTVNRVTVVHYHYTVEDGADIALLELEIPVNVSTHPIPLPASPSTFGTSCWYTG 159
 QY 190 GYIKEDALPSPHTLOEVOVAIIINSMCNHLFLKYSFRKD-----IFGDMVCAGNAQGGK 245
 Db 160 GDIDSEDELLFPYPLKQVKPIVENSCLDRKYHTGLYTGDDVPVQDGMLCAGNTR--SD 217
 QY 246 ACFGDSGGPLACNKNGLWYQGVSWGVGCGRRPGRVYTNISHHFEWIKLMAQ 300
 Db 218 SCQDSGGGLCKVKGWTLQAGVSWGEGCAENRPGIYTRYVYLDWIHYVPQ 272

RESULT 14
 KFHUI
 coagulation factor Xia (EC 3.4.21.27) precursor [validated] - human
 N:Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
 C:Species: Homo sapiens (man)
 C>Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-Dec-2000
 C:Accession: A27431; A00920; A37940
 R:Asakai, R.; Davie, E.W.; Chung, D.W.
 Biochemistry 26, 7221-7228, 1987
 A:Title: Organization of the gene for human factor XI.
 A:Reference number: A27431; MUID:88107663; PMID:2827746
 A:Accession: A27431
 A:Molecule type: DNA
 A:Residues: 1-625 <ASA>
 A:Cross-references: GB:M18295
 A>Note: the sequence shown follows the authors' translation
 R:Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
 Biochemistry 25, 2417-2424, 1986
 A:Title: Amino acid sequence of human factor XI, a blood coagulation factor with four ta
 A:Reference number: A00920; MUID:86243360; PMID:3636155
 A:Accession: A00920
 A:Molecule type: protein
 A:Residues: 1-625 <FU>
 A:Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
 R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
 Biochemistry 30, 2056-2060, 1991
 A:Title: Location of the disulfide bonds in human coagulation factor XI: the presence of
 A:Reference number: A37940; MUID:91152017; PMID:1998667
 A:Accession: A37940
 A:Molecule type: protein
 A:Residues: 28-33;35-49, 'X', 51-55, 'X', 57-63;70-75, 'X', 77-79;107-109, 'X', 111-112;132-139,
 ;280-282, 'X', 284;285-297;313-316, 'X', 318-319;320-326, 'X', 328-330, 'X', 347-349;373, 'X', 375
 C:Comment: The proenzyme consists of two identical chains linked by one or more disulfid
 he active site, and a heavy chain, which associates with high molecular weight (HMW) kin
 C:Genetics:
 A:Gene: GDB:F11
 A:Cross-references: GDB:119891; OMIM:264900
 A:Map position: 4q35-4q35
 A:Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor IX
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor XI; trypsin homology
 C:Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:19-387/Product: coagulation factor Xia heavy chain #status experimental <HCH>
 F:19-108/Domain: apple repeat <AP1>
 F:109-198/Domain: apple repeat <AP2>
 F:199-288/Domain: apple repeat <AP3>
 F:290-379/Domain: apple repeat <AP4>

F:388-625/Product: coagulation factor Xia light chain #status experimental <LCH>
 F:388-618/Domain: trypsin homology <TRY>
 F:20-103,514-581,571-599/Disulfide bonds: #status predicted
 F:29/Disulfide bonds: interchain #status experimental
 F:46-76,50-56,110-193,136-165,140-146,200-283,226-255,230-236,291-374,317-346,321-327,3
 F:90,126,353,450/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:339/Disulfide bonds: interchain #status predicted
 F:387-388/Cleavage site: Arg-Ile (coagulation factor XiiA) #status experimental
 F:431,480,575/Active site: His, Asp, Ser #status predicted
 F:491/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 27.0%; Score 483.5; DB 1; Length 625;
 Best Local Similarity 41.0%; Pred. No. 3 3e-35;
 Matches 103; Conservative 39; Mismatches 86; Indels 23; Gaps 8;

QY 51 ITRIVGGDEAELGRWFWQGSRL---WDHVGCVLLSHRWALTAHCF---EYYSDL 104
 Db 384 IKPRIVGGTASVRGEPWQVTLHTTPTQRHLGCGSIIGNQWILTAHCFYGVESPKILR 443
 QY 105 DPGVMWQFGQLTSPFSWLSQAYTRYFVSNILSPRY-LGNSPYDIALVKLSAPVY 163
 Db 444 VYSGILNQ-SEIKEDTSFVGQ-----EIIHDQYKMAESGYDIALKLETVYNT 493
 QY 164 KHIQPIQLQASTFEFENRTDCWYTKNGYIKEDALPSPHTLOEVOVAIIINSMCNHLFLK 223
 Db 494 DSQRPICLPSKGRNVITYDQWVTGWYRKLKDKI--QNTLQKAKIPLVTNECQK--R 548
 QY 224 YSFRKDIIFGDMVCAGNAQGGKDACFGDSGLACNKNGLWYQGVSWGVGCGRRPGRV 283
 Db 549 YRGHK-ITHKMICAGYREGGKDACGDSGLPUSCKHNEVHVLVGTSMGEGCAQRERPGV 607
 QY 284 YTNISHHFEW 294
 Db 608 YTNVVEYVDVI 618

RESULT 15
 S00845
 hepsin (EC 3.4.21.-) - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
 C:Accession: S00845
 R:Leytus, S.P.; Loeb, K.R.; Hagen, F.S.; Kurachi, K.; Davie, E.W.
 Biochemistry 27, 1067-1074, 1988
 A:Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane do
 A:Reference number: S00845; MUID:88209431; PMID:2835076
 A:Accession: S00845
 A:Molecule type: mRNA
 A:Residues: 1-417 <LEV>
 A:Cross-references: EMBL:X07732; NID:g32063; PIDN:CAA30558.1; PID:g32064
 C:Genetics:
 A:Gene: GDB:HPN; TMAPRSL; hepsin
 A:Cross-references: GDB:135685; OMIM:142440
 A:Map position: 19q11-19q13.2
 C:Superfamily: hepsin; trypsin homology
 C:Keywords: hydrolase; liver; serine protease; transmembrane protein
 F:23-45/Domain: transmembrane #status predicted <TM>
 F:163-400/Domain: trypsin homology <TRY>
 F:188-204,291-329,322-338,349-381/Disulfide bonds: #status predicted
 F:203,257,353/Active site: His, Asp, Ser #status predicted

Query Match 26.6%; Score 477.5; DB 1; Length 417;
 Best Local Similarity 41.1%; Pred. No. 7e-35;
 Matches 115; Conservative 30; Mismatches 96; Indels 39; Gaps 11;

QY 34 PSQEAAPLSPGCGRRVI-TSRIVGDEAELGRWFWQGSRLRWDHVGCVLLSHRWALT 92
 Db 141 PRGRFLAICQDCGRKLPVDRVGRDTSLSGRWFWQVSLRWDHVGCVLLSGDWILT 200
 QY 93 AAHCETYSYDLSDPGVMWQFGQLTSPFSWLSQ-----AYTRYFVSNILSPRYLGN 146
 Db 201 AAHCFFERNRL--SRNRV-FAGAVAAQSPHGLQGVQAVVTHGGYLP---FRDPNSEN 254

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OM protein - protein search, using sw model

Run on: April 6, 2004, 14:09:09 ; Search time 45 Seconds
(without alignments)
2292.766 Million cell updates/sec

Title: US-09-787-844-2
Perfect score: 1792
Sequence: 1 RQRGRQAGEAMGARGNL.....PSWPLLPFLWALPLGPV 327

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_rhco:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_protist:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178	65.7	336	11 Q80YD8	Q80YD8 mus musculus
2	1123.5	62.7	328	11 Q80Z40	Q80Z40 rattus norv
3	845	47.2	322	11 Q920S2	Q920S2 mus musculus
4	812	45.3	282	11 Q9D4I3	Q944I3 mus musculus
5	602	33.6	321	4 Q96RZ8	Q96RZ8 homo sapien
6	580.5	32.4	389	13 Q9PVX7	Q9PVX7 xenopus lae
7	580	32.4	328	11 Q8BJR6	Q8BJR6 mus musculus
8	572.5	31.9	311	11 Q80XZ3	Q80XZ3 rattus norv
9	571.5	31.9	331	11 Q8R1A6	Q8R1A6 mus musculus
10	568.5	31.7	331	11 Q80X17	Q80X17 mus musculus
11	565.5	31.6	339	11 Q9SL44	Q9SL44 mus musculus
12	561	31.3	337	13 Q9DGR3	Q9DGR3 xenopus lae
13	550	30.7	340	11 Q8BJV6	Q8BJV6 mus musculus
14	534.5	29.8	307	11 Q7TML0	Q7TML0 mus musculus
15	533.5	29.8	297	11 Q88781	Q88781 rattus ratt
16	532.5	29.7	310	11 Q91XC4	Q91XC4 mus musculus

17	524.5	29.3	310	11 Q9QYZ9	Q9QYZ9 mus musculus
18	522.5	29.2	471	11 Q8CFE0	Q8CFE0 mus musculus
19	522	29.1	273	6 Q9XSM1	Q9XSM1 ovis aries
20	516.5	28.8	568	4 Q86YM4	Q86YM4 homo sapien
21	515.5	28.8	581	4 Q9BYE2	Q9BYE2 homo sapien
22	515	28.7	275	4 Q96RZ6	Q96RZ6 homo sapien
23	512.5	28.6	537	4 Q9BYE1	Q9BYE1 homo sapien
24	512	28.6	417	11 Q8BZ10	Q8BZ10 mus musculus
25	511.5	28.5	257	11 Q8BZ04	Q8BZ04 mus musculus
26	511	28.5	320	13 Q770X2	Q770X2 xenopus lae
27	510	28.5	643	6 Q97506	Q97506 sus scrofa
28	509	28.4	273	11 Q921N4	Q921N4 mus musculus
29	508.5	28.4	638	11 Q80P55	Q80P55 mus musculus
30	506	28.2	277	11 Q80WM7	Q80WM7 mus musculus
31	506	28.2	453	11 Q81ZAG	Q81ZAG mus musculus
32	504	28.1	624	11 Q9DAT3	Q9DAT3 mus musculus
33	502	28.0	624	11 Q91Y47	Q91Y47 mus musculus
34	501	28.0	275	4 Q86TM8	Q86TM8 homo sapien
35	501	28.0	276	4 Q86UA5	Q86UA5 homo sapien
36	500.5	27.9	767	13 Q9DGR2	Q9DGR2 xenopus lae
37	497.5	27.8	327	4 Q8N171	Q8N171 homo sapien
38	496.5	27.7	284	4 Q8NF86	Q8NF86 homo sapien
39	496.5	27.7	329	13 Q42272	Q42272 xenopus lae
40	493.5	27.5	371	11 Q8CJ16	Q8CJ16 rattus norv
41	493.5	27.5	445	11 Q8CJ17	Q8CJ17 rattus norv
42	491	27.4	271	6 Q8HVJ2	Q8HVJ2 bos taurus
43	489.5	27.3	293	4 Q7Z5A4	Q7Z5A4 homo sapien
44	486.5	27.1	455	11 Q8CDR0	Q8CDR0 mus musculus
45	486	27.1	855	4 Q7Z410	Q7Z410 homo sapien

ALIGNMENTS

RESULT 1

Q80YD8 PRELIMINARY; PRT; 336 AA.
ID Q80YD8;
AC Q80YD8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to protease, serine, 21 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049588; AAH49588.1;
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:004235; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Src; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
FT NON TER 1
SQ SEQUENCE 336 AA; 37361 MW; E5206FEDBE55C670 CRC64;

Query Match 65.7%; Score 1178; DB 11; Length 336;
Best Local Similarity 64.7%; Pred.No. 1.6e-101;
Matches 218; Conservative 40; Mismatches 63; Indels 16; Gaps 4;


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QY 182 TDQVTCGWYKED-EALPSPHTLOEVQVVAIINNMCNHLFLKYSFRKDFGDMVCAGNA 240
DB 176 PRQVTCGWYKEDLKPFPYHLREVQVQSILNNSRCQELFEISSLHLITKDVFCAGAE 235
QY 241 QGQKDACFGDSGGLACNKNGLWYQIGVSWGVCGRNRPQVYTNISHHFEWIKLMAQ 300
DB 236 DGSADICGDSGGLVLCNMDGLWYQIGVSWGVCGRNRPQVYTNISHHFEWIKLMAQ 295
QY 301 SGMSQPDPSWPLFFPFLWALPLLP 326
DB 296 NGAVRRDLALPILLSITLLQAPWLLRP 321

RESULT 4
Q9D413 PRELIMINARY; PRT; 282 AA.
AC Q9D413
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE 4931440B09Rik protein.
GN 4931440B09Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akazawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirrl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayaehizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK016509; BAB30277.1; -
DR HSSP; P00763; IDPO.
DR MSROPS; S01.417; -.
DR MGD; MGI:1918253; 4931440B09Rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 282 AA; 31997 MW; 48D89B74F750BAB4 CRC64;

Query Match 45.3%; Score 812; DB 11; Length 282;
Best Local Similarity 54.9%; Pred. No. 1.8e-67;

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Matches 156; Conservative 40; Mismatches 82; Indels 6; Gaps 4;
QY 45 PCGRVIT-SRIVGEDAELGRWPQGSRLRLWDSHVCSVLSHRWALTAHCFETYSDL 103
DB 2 PCGRNDRSRIVGVISMGQRNFWQASRLRLKSHRCGSLSSRWVLTAAHCFKY--- 58
QY 104 SDPSGWMVQFQLTSMFWSLQAYTRYFVSNIYLSFRLGNSPYDIALVKLSAPVYIT 163
DB 59 LDPEKWTYQLQGLTSKPSYNNRKAYSGRYRVKDIIVNSEDKLS-HDLALLRLASSVYN 117
QY 164 KHQIPICLOASTFEFNRTDCWVTGWYKED-EALPSPHTLOEVQVVAIINNMCNHLFL 222
DB 118 KDQPVCVQSTFTSQHQPCWVTGWYKEDLKPFPYHLREVQVQSILNNSRCQELFE 177
QY 223 KYSFRKDFGDMVCAGNAQGGKDACFGDSGGLACNKNGLWYQIGVSWGVCGRNRPQ 282
DB 178 IFSLHLITKDVFCAGAEADGSDATCSGDSGGLVLCNMDGLWYQIGVSWGVCGRNLP 237
QY 283 VYTNISHHFEWIKLMAQSGMSQPDPSWPLFFPFLWALPLLP 326
DB 238 IYTNVSHYNIETWMLNGAVRRDLALPILLSITLLQAPWLLRP 281

RESULT 5
Q96RZ8 PRELIMINARY; PRT; 321 AA.
AC Q96RZ8
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE HS transmembrane tryptase, gene name TWT, AF175522.1.
GN TRPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21095910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgins D.R.;
RA "Sequence, structure and pathology of the fully annotated terminal 2
RA Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AE006466; AAK61269.1; -.
DR HSSP; P00761; IAN1.
DR GO; GO:0001602; C:integral to membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease; Transmembrane.
SQ SEQUENCE 321 AA; 33829 MW; FFF5089EDC4FC73D CRC64;

Query Match 33.6%; Score 602; DB 4; Length 321;
Best Local Similarity 42.9%; Pred. No. 8.5e-48;
Matches 140; Conservative 40; Mismatches 98; Indels 48; Gaps 11;
QY 13 AMGARGALLIALLARAGLRKPSQEAAPISGPGCRVIT---SRIVGEDAELGRWPQ 69
DB 2 ALGACG-LLILLAVFGVSLR-----TLQPGCRFQVSDAGRVGGHAAPAGWPWQ 52
QY 70 GSLRLWDSHVCSVLSHRWALTAHCFETYSDLSDPSGWMVQFQL--TSMPSFWSLQA 127

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Db 53 ASLRRLRVHVCGLSLSPQWLTAAHCFSGSLNSD---YQVHLELEITLSPHFSTVRQ 109
QY 128 YTRYFVSNIVLSPRYLGNSPVDIALVKLSAPVTVTKHIQICLOASTFEENRTDCWVT 187
Db 110 II-----LHSSPSGQGTSCDIALVELSVPTLSSRLFPVCLPEASDPCPCGIRCWVT 162
QY 188 GWYIKEDALPSPHTLOEVQVAIINNMCNHLFLKYSFRKDFG-----DMVCAGN 239
Db 163 GWYITREGEPLPPYSLREVKVSVDVDTCTC-----RDYFPGGSLQPDMLC--- 210
QY 240 AQGGKACFGSGGGLACNKLNGLYQIGVSWGCGRPNRPVYTNISHHFWIQLMA 299
Db 211 ARGPGDACCDDSGGLVCQVNGAWQAGIVSWGCGRPNRPVYTRVPAIVNVIRRHIT 270
QY 300 QSGMSQPD-PSWPLL---FFPLLWAL 321
Db 271 ASGSGESGPRPLLAGFPLFLGL 296

RESULT 6
Q3PVX7 PRELIMINARY; PRT; 389 AA.
AC Q3PVX7;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Epidermis specific serine protease.
GN XEPSIN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K.;
RT "The expression control of xepsin by non-axial and planar
RT posteriorizing signals in Xenopus epidermis.";
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB018694; BAA84941.1; -.
DR HSSP; P00763; 1DPO.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 389 AA; 42375 MW; B1FBA42F5D1F6E3 CRC64;

Query Match 32.4%; Score 580.5; DB 13; Length 389;
Best Local Similarity 40.2%; Pred. No. 1.1e-45;
Matches 121; Conservative 43; Mismatches 84; Indels 53; Gaps 7;

QY 46 GRRVITRIYGGDAELGRNFWQGLSLWDSHVYGVLSLHSHRWALTAACFFETYS----- 101
Db 17 CCVPVISHRIYVGMDSKKGFWQGLSISYKSDSICGGLSLTDSWMTAAHCIDSLDVSYY 76
QY 102 -----DLSDPSGMWVQF--QLTSMPSFWSLQAYTRYFVSNIVLSPRYLGNSPVDIA 152
Db 77 TVVLGAYQLSADPNSTVSRGVKSIKHPDF-----QYEGSSG-DIA 116
QY 153 LVKLSAPVTVTKHIQICLOASTFEENRTDCWVTGWYIKEDALPSPHTLOEVQVAII 212

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Db 117 LIELEKPVTVTFYILPICLPSSQDVQFAAGTMCWTVGWNIGBETFLISPKTIQKAEVAII 176
QY 213 NNSMCNHLFLK-----YSFRKDFGDMVCAGNAQGGKDACFGDSGGPLACNKLNGLYQ 265
Db 177 DSVCGTMYESSLGVIPDFSFQIE---DMVCAGYKEGRIDACQDGGGGLVCNVNWLQ 233
QY 266 IGVVSWGVCGRPNRPVYTNISHHFWIQLMAQSGMSQPDPSWPLLFFPLLWALPLL 325
Db 234 LGIVSNGYCAEPNRPVYTVKQYQDWLKTIVPLVFSSEGGFS-----VAPSIG 283
QY 326 P 326
Db 284 P 284

RESULT 7
Q8BJR6 PRELIMINARY; PRT; 328 AA.
AC Q8BJR6;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to MARAPsin precursor (Channel-activating protease 2-like
DE protein) (Pancreasin).
GN MPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=12986/SvEvTac;
RC Brathwaite M., Waeltz P., Schlessinger D., Nagaraja R.;
RT "Genomic Sequence Analysis in the Mouse T-complex Region.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Bladder;
RX MEDLINE=22439795; PubMed=12441343;
RA Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Wolters P.J.,
RT Caughey G.H.;
RT "Structure and activity of human pancreasin, a novel tryptic serine
RT peptidase expressed primarily by the pancreas.";
RL J. Biol. Chem. 5:3363-3371 (2003).
DR EMBL; AK080281; BAC37864.1; -.
DR EMBL; AY162410; AA017162.1; -.
DR EMBL; AF542056; AA027572.1; -.
DR MGD; MGI:2450523; Mpn.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Protease.
SQ SEQUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;

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Query Match 32.4%; Score 580; DB 11; Length 328;
Best Local Similarity 43.8%; Pred. No. 9.9e-46;
Matches 128; Conservative 42; Mismatches 94; Indels 28; Gaps 8;

QY 19 ALLALLARAGLRKPSQEAAPLSGCGRRVITSRIYGGEDAEALGRWPQGSRLWDSH 78
DB 8 ALLLLPLLRSG-----TEGARLRACGPKPMFNWVGGENALEGEWPNQVSIQRNGH 61

QY 79 VCGVSLLSHRWALTAACHFTYSDLSDPGSMVQFQGLTSMPSFWSLQ-----AYTRYF 133
DB 62 FCGSLIAPTWLTAAHCF---SNTSDISYQLLGLAL-----KLQPGPHALYVP-- 109

QY 134 VSNILSPRYLG-NSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDQWTCGWYI 192
DB 110 VKQKSNFQVQWASSADVALVQLQGVTFNVLVCLPDPSPVIFESGMNMTWVGSP 169

QY 193 KEDEALPSPTLQEVQVAINNMCNHLF---LKYGFR-KDIFGDMVCAGNAQGGKDACF 248
DB 170 SEQDRLENPRVLOKLAVIDTPKCNLLYNKDVESDFOLKTKDDMLCAGFAEGKDAC 229

QY 249 GDSGGPLACNKGWLTQIGVSVGCGRRNRPVYTNISHHPEWTKLMAQ 300
DB 230 GDSGGPLVCLVDQSWQAGVISWEGCARRNRPVYRTVSHHKKWIIHQIPE 281

RESULT 8
Q80XZ3 PRELIMINARY; PRT; 311 AA.

ID Q80XZ3
AC Q80XZ3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Trypase gamma 1.
GN TP8G1.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Li L., Wong G.W., Yang Y., Stevens R.L.;
RT "Identification of rat trypase gamma hydrophobic extension."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY196208; AAC00840.1; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 311 AA; 32807 MW; 78362611679398FF CRC64;

Query Match 31.9%; Score 572.5; DB 11; Length 311;
Best Local Similarity 41.7%; Pred. No. 4.6e-45;
Matches 129; Conservative 39; Mismatches 112; Indels 29; Gaps 8;

QY 24 LLLARAGLRKPSQEAAPLSGCGRRVITSRIYGGEDAEALGRWPQGSRLWDHVCVGS 83
DB 11 LLLAVGCGQPVSHAG-----SRIVGHAQAQAWPQASLRILQKVHVCVGS 58

QY 84 LLSHRWALTAACHFTYSDLSDPGSMVQFQGLTSMPSFWSLQAYTRYFVSNILSPRY 143
DB 59 LLSPEWLVLTAAHCFSSVNSD---YEVHLGLTLT-----TLSPFSTVKQIIWSSAPG 110

QY 144 LGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDQWTCGWYIKDEALPSPT 203
DB 111 PFGSGDIALVQLATPVALSSQVQVCLPEASADFPHGQWTCGWYIQSGEPLKPPYN 170

QY 204 LOEVQVAINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGGPLACNKGW 263
DB 171 LOEAKVSVVDVETCSQAY-SSNGSLIQSDMLC---AWPGDACODDSDGGPLVCRVAGIW 226

QY 264 VOIGVSVGCGRRNRPVYTNISHHPEWTKLMAQSGMSQDPSH-PL---LFFPLL 318
DB 227 QQAGVSVGCGRRNRPVYTNISHHPEWTKLMAQSGMSQDPSH-PL---LFFPLL 318

QY 319 WALPLLGEV 327
DB 287 FILLVSGVV 295

RESULT 9
Q8RIAG PRELIMINARY; PRT; 331 AA.

ID Q8RIAG
AC Q8RIAG
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RIKEN CDNA 2010001P08 gene.
GN 2010001P08RIK.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024903; AAH24903.1; -
DR HSP; P00761; IAN1.
DR MGB; MGI:1917064; 2010001P08RIK.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 331 AA; 35639 MW; C06F6EF2FA261636 CRC64;

Query Match 31.9%; Score 571.5; DB 11; Length 331;
Best Local Similarity 42.8%; Pred. No. 6.2e-45;
Matches 127; Conservative 36; Mismatches 101; Indels 33; Gaps 7;

QY 42 LSGPCGRRVITSRIYGGEDAEALGRWPQGSRLWDHVCVSLSHRWALTAACHFTYS 101
DB 41 LDSVCGRRPRTSGRIVSGQDQALGRWPQVSVRENGAHVCGSLIADWVLTAACHFNQ 100

QY 102 DLSDPSCMWVQFQGLTSMPSF---WSLQAYTRYFVSNILSPRYLG--NSPYDIALVK 156
DB 101 SLST---YTVLLGTISYPEDNEPKELRA-----VAQFKHPSYADSHSSGDIALV 151

QY 157 SAPVYTKHIQICLOASTFEFENRTDQWTCGWYIKDEALPSPTLQEVQVAINNMS 216
DB 152 ASPISFNDYMLPVCLPKPGDPLDPGTMCTWGTGWHIGTQCLPPLPPTLQELQVPLDAET 211

QY 217 CNHLFLKYSF---RKIDFGDMVCAGNAQGGKDACFGDSGGPLACNKGWYIQGVSWGV 273
DB 212 CNTYOENSTPGTEPVILEGMLCAGPQGGKDACNGSDGGLVCDINDWVIAQGVSWGS 271

QY 274 GCGRRNRPVYTNISHHPEWTKLMAQSGMSQDPSWPLL-----FFPLLWALPLAG 325
DB 272 DCALFKRPVYTNVSYISWIKNTY-----WNLPMGRGSPSLSGTFLUG 317

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Embryonic serine protease-1.
 GN XESP-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20363741; PubMed=10903452;
 RX Yamada K., Takabatake T., Takehima K.;
 RA "Isolation and characterization of three novel serine protease genes
 from Xenopus laevis".
 RT Gene 252:209-216(2000).
 RL EMBL; AB038496; BAB08216.1; -.
 DR HSSP; P00763; 1DPO.
 DR MEROPS; S01.048; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR003003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 317 AA; 34413 MW; BEC78A9F46D138FE CRC64;
 Query Match 31.3%; Score 561; DB 13; Length 317;
 Best Local Similarity 41.5%; Pred. No. 5.6e-44;
 Matches 127; Conservative 34; Mismatches 105; Indels 40; Gaps 9;
 QY 39 AAPLSPGCGRRVITSRIVGGDAELGRWPQGSRLWDSHVGVSLLSHRWALTAHCFE 98
 DB 28 APPL---CSSPFSSRIVGDTTRQGANPWQSLFENGSHICGSLISDQWILTAHCIE 84
 QY 99 TVSDLSPPSGMWVQFQCLTSMPSFNSLQAYTRYFVSN-----IYLSPLYG-NS 147
 DB 85 -HPDL-PSGCGVRLG-----AY--QLYVKNPHEMTVKVDIIYINSEFNGPQT 127
 QY 148 PYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWTGNGYKEDEALPSPTLQEV 207
 DB 128 SGDIALLKUSSPIKFTYELIPLCLPASPTFSGTECTIGWGQTSVPLQYPATLOKV 187
 QY 208 QVAIINNSMCHLFLKYSFRKD---IFGDMVCAGNAQGGKACFGDSGGGLACNKGILW 263
 DB 188 MYPILNRDCEKMYHINSVISETEILLQSDICAGYQAGKQCGDGGPLVCKIQGF 247
 QY 264 YQIGVSVWGCGGRPNRPGVYTNISHHFWIKLMAQS-----GMSQDDPSWPLFFPL 318
 DB 248 YQAGIVSWGERCAKRNPGVYTFVPAYETWISERSVISFKPTSSSSPSVLRASAIL 307
 QY 319 WALPL 324
 DB 308 LGVSL 313
 ID Q8BJV6 PRELIMINARY; PRT; 340 AA.
 AC Q8BJV6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Proctasin.

GN PRSS8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Eye;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs".
 RL Nature 420:563-573(2002).
 DR EMBL; AK078636; BAC37362.1; -.
 DR MGD; MGI:1923810; Prss8.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR003003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 SQ SEQUENCE 340 AA; 38503 MW; 3C2540E9B3A81C8A CRC64;
 Query Match 30.7%; Score 550; DB 11; Length 340;
 Best Local Similarity 37.4%; Pred. No. 6.5e-43;
 Matches 131; Conservative 57; Mismatches 88; Indels 74; Gaps 14;
 QY 20 LLLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGDAEL-GRWPQGSRLWDSH 78
 DB 17 ILDLLGLQSGIR-ADGTEAS-----CG-AVIQRTGGQGWSPGQMPQVSTYDGNH 69
 QY 79 VCGVSLLSHWALTAHCF-----ETYSDLSPSGMWVQFQCLTSMPSFNSLQAYTRY 132
 DB 70 VCGSVLSVSNKWSVSAHCFREHSREAYE-----VKLGD-----HQLDSY---- 109
 QY 133 FVSN---IYLSPLYGNSPY-----DIALVKLSAPVYTKHIQICLOASTFEFENRT 182
 DB 110 --SNDTVHTVAQIITHSSYRESGQGDIALIRLSPVTFESYRIRPCLPAANASFPNGL 167
 QY 183 DCWTGNGYKEDEALPSPTLQEVQVAIINNSMCHLFLKYSFRKD---IFGDMVCAGN 239
 DB 168 HCTVTGNGHVAHSVLTQPRPQQLEVPILSRCTSCLYNINAVPEPHTIQDMLCAGY 227
 QY 240 AQGKDACFGDSGGPLACNKGILWYQIGVSVWGCGGRPNRPGVYTNISHHFWIQ---- 295
 DB 228 VKGKDACQCGDSGGLSCPMEGIWYLAGIVSGDACGAPNPGVYTLTSTYASWTHHVA 287
 QY 296 ----KLMAQSGMSQPD-----PSW-----PLLPFLPLWALPLL 324
 DB 288 ELQPRVVPQTQESQPDGHLNHHVPFSSAAAPKLLRPVLPFLPLGLTLGLL 337
 RESULT 14
 Q7TML0
 ID Q7TML0 PRELIMINARY; PRT; 307 AA.
 AC Q7TML0;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RIKEN cDNA 4733401N09.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant I.B., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iaquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055854; AAH55854.1; --
SQ SEQUENCE 307 AA; 33431 MW; 58692F29355B704E CRC64;

Query Match 29.8%; Score 534.5; DB 11; Length 307;
Best Local Similarity 38.4%; Pred. No. 1.6e-41;
Matches 114; Conservative 53; Mismatches 103; Indels 27; Gaps 6;

QY 20 LLLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEDAEGLRWPMQGLRLWDSHV 79
DB 19 ILLVLLTSTA-----PISAAITRVSPDCGKPOQLNRIVGGEDSDMDAQPMWIVSLKNGSHH 74
QY 80 CGVSLLSHRWALTAACFETYSIDLSPSGMWVQFGLTSMPSFWSLQAYTR---YFVSN 136
DB 75 CAGSLTLNRVVTAAACFK--SNMDKPSLPSVLLGA-----WKLGPSPRSQKVGIAW 125
QY 137 IYLSPRY--LGNSPYDIALVKLSAPVTYTKHIQICLQASTFEFENETDCWVTGWGIKE 194
DB 126 VLPHRYGKNGKSTHADIALLVLEHSIQFSEILPCLPDSVRUPPKTDICWAGWSIQD 185
QY 195 DEALPSPHTLQEVQVAIINNSCNHLFLKYFRKDIIFGDMVCAGNAQGGKDACFGDSGGP 254
DB 186 GVPLPHTQTLQKLVPIIDSELCKSLYWRGAGQEAITEGMLCAGYLEGERDACLDGSGP 245
QY 255 LACNKGWLYQIGVVSNGVCGRRNRPQVYVNIHSHFEWIOKL-----MAQSG 302
DB 246 LMCQVDHLLTGLTIISWGEGCAERNRPGVYVTSLLAHRVQVRIQVQVQLRGLADSG 302

RESULT 15
O88781 PRELIMINARY; PRT; 297 AA.
AC O88781
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine protease precursor (Fragment).
GN BSP2.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fishier; TISSUE=Brain;
RX MEDLINE=98389725; PubMed=972524;
RA Davies B.J., Fickard B.S., Steel M., Morris R.G., Lathe R.;
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RT "Serine Proteases in Rodent Hippocampus.";
RL J. Biol. Chem. 273:23004-23011 (1998).
DR EMBL; AJ005642; CAA06644.1; --
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.252; --
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KW Hydroxylase; Protease; Serine protease; Signal.
FT NON_TER 1 1
FT SIGNAL <1 23 POTENTIAL.
FT CHAIN 24 297 SERINE_PROTEASE.
SQ SEQUENCE 297 AA; 32086 MW; 6DA25C6633D6AB55 CRC64;

Query Match 29.8%; Score 533.5; DB 11; Length 297;
Best Local Similarity 37.5%; Pred. No. 1.9e-41;
Matches 115; Conservative 55; Mismatches 102; Indels 35; Gaps 8;

QY 16 ARGA----LLALLARAGLRKPESQEAAPLSPG--PCGRRVITSRIVGGEDAEGLRWPMQ 69
DB 1 ARGSSPPGLTLFILLPSA-----TVSAANIRGSPDCGKPOQLNRIVGGEDSADAQPMWI 54
QY 70 GSLRLWDSHVCGVSLLSHRWALTAACFETYSIDLSPSGMWVQFGLTSMPSFWSL---Q 126
DB 55 VSILKNGSHHCAGSLTLNRVVTAAACFKS--SNMDKPSFYSVLLGA-----WKLGNPG 105
QY 127 AYVTRYFVSNIYLSPRY--LGNSPYDIALVKLSAPVTYTKHIQICLQASTFEFENETDC 184
DB 106 PRSQKVGIASVLPHPRYSRKSTHADIALLVLERIQFSEAILPCLPDSVSLPPNTNC 165
QY 185 WYTGWGYIKEDBALPSPHTLQEVQVAIINNSCNHLFLKYFRKDIIFGDMVCAGNAQGGK 244
DB 166 WIAGWSIQDGVLPRLPQTLQKLVPIIDPELCKSLYWRGAGQEAITEGMLCAGYLEGR 225
QY 245 DACFGDSGGPLACNKGWLYQIGVVSNGVCGRRNRPQVYVNIHSHFEWIOKL----- 297
DB 226 DACLDGSGGLCMQVDHLLTGLTIISWGEGCAERNRPGVYVTSLLAHRVQVRIQVQVQLR 285
QY 298 --MAQSG 302
DB 286 GRLADSG 292

Search completed: April 6, 2004, 14:13:05
Job time : 47 secs
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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1728	96.4	314	9	US-09-909-320-257		Sequence 257, App
2	1728	96.4	314	9	US-09-885-441-14		Sequence 14, App
3	1728	96.4	314	9	US-09-909-088B-257		Sequence 257, App
4	1728	96.4	314	9	US-09-905-391A-257		Sequence 257, App
5	1728	96.4	314	9	US-09-902-853-257		Sequence 257, App
6	1728	96.4	314	9	US-09-907-824-257		Sequence 257, App
7	1728	96.4	314	9	US-09-907-841-257		Sequence 257, App
8	1728	96.4	314	10	US-09-904-011-257		Sequence 257, App
9	1728	96.4	314	10	US-09-906-742-257		Sequence 257, App
10	1728	96.4	314	10	US-09-906-638-257		Sequence 257, App
11	1728	96.4	314	10	US-09-907-613-257		Sequence 257, App
12	1728	96.4	314	10	US-09-907-942-257		Sequence 257, App
13	1728	96.4	314	10	US-09-904-859-257		Sequence 257, App
14	1728	96.4	314	10	US-09-909-204-257		Sequence 257, App
15	1728	96.4	314	10	US-09-904-820-257		Sequence 257, App

PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,598
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-257

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Mismatches 0; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGDEAELGRWPWQSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGDEAELGRWPWQSLR 60
QY 74 LWDHVCVGSLLSHRWALTAACHFETYSDDLSDPSGVMVQFGLTSMPSFWSLQAYTRYF 133
DB 61 LWDHVCVGSLLSHRWALTAACHFETYSDDLSDPSGVMVQFGLTSMPSFWSLQAYTRYF 120
QY 134 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGMYIK 193
DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGMYIK 180
QY 194 EDEALPSHTLQEVQVAIIINSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSHTLQEVQVAIIINSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKNGLWQIGVVSVMGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSPWPLL 313
DB 241 PLACNKNGLWQIGVVSVMGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSPWPLL 300
QY 314 FPFLWALPLGVPV 327
DB 301 FPFLWALPLGVPV 314

RESULT 2
US-09-885-441-14
Sequence 14, Application US/09885441
Patent No. US20020146407A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong

TITLE OF INVENTION: Regulation of Human Eosinophil Serine
TITLE OF INVENTION: Protease-1-Like Enzyme
FILE REFERENCE: 04974.00512
CURRENT APPLICATION NUMBER: US/09/885,441
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/212,844
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/244,171
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US 60/279,766
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-09-885-441-14

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Mismatches 0; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGDEAELGRWPWQSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGDEAELGRWPWQSLR 60
QY 74 LWDHVCVGSLLSHRWALTAACHFETYSDDLSDPSGVMVQFGLTSMPSFWSLQAYTRYF 133
DB 61 LWDHVCVGSLLSHRWALTAACHFETYSDDLSDPSGVMVQFGLTSMPSFWSLQAYTRYF 120
QY 134 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGMYIK 193
DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVITYTKHIQPICLQASTFEFFENRTDCWVTGMYIK 180
QY 194 EDEALPSHTLQEVQVAIIINSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALPSHTLQEVQVAIIINSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKNGLWQIGVVSVMGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSPWPLL 313
DB 241 PLACNKNGLWQIGVVSVMGCGRRNRPVYTNISHHFEWIKLMAQSGMSQPPSPWPLL 300
QY 314 FPFLWALPLGVPV 327
DB 301 FPFLWALPLGVPV 314

RESULT 3
US-09-909-088B-257
Sequence 257, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerriksen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-257

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLIARAGLRKPSQEAAPLSGPGRRVITSRIVGGDEALGRWPQGSRLR 73
DB 1 MGARGALLALLIARAGLRKPSQEAAPLSGPGRRVITSRIVGGDEALGRWPQGSRLR 60

QY 74 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDSGMMWQFQGLTSPFWSLQAYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDSGMMWQFQGLTSPFWSLQAYTRYF 120

QY 134 VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRDCWVTGWGVIK 193
DB 121 VSNYILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRDCWVTGWGVIK 180

QY 194 EDALSPSPHTLOEQVAIVAINNSCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDALSPSPHTLOEQVAIVAINNSCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240

QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 313
DB 241 PLACNKNGLWYQIGVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

QY 314 FFPLLWALPULGPV 327
DB 301 FFPLLWALPULGPV 314

RESULT 4
US-09-905-291A-257
Sequence 257, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrata, Napoleone
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911

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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-257

Query Match          96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 60

QY 74 LWDHSHVCGVSLSHRWALTAHCFETYSYDLSDPGGMVQFGLTSMPSFWSLQAYYTRYF 133
Db 61 LWDHSHVCGVSLSHRWALTAHCFETYSYDLSDPGGMVQFGLTSMPSFWSLQAYYTRYF 120

QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGYIK 193
Db 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGYIK 180

QY 194 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAAGQKDACFGDSGG 253
Db 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAAGQKDACFGDSGG 240

QY 254 PLACNKNGLWYQIGVSWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 313
Db 241 PLACNKNGLWYQIGVSWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300

QY 314 FFPLLWALPLIGPV 327
Db 301 FFPLLWALPLIGPV 314
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RESULT 5

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US-09-902-853-257
; Sequence 257, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tomas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-257
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Query Match          96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPWGSLR 60

QY 74 LWDHSHVCGVSLSHRWALTAHCFETYSYDLSDPGGMVQFGLTSMPSFWSLQAYYTRYF 133
Db 61 LWDHSHVCGVSLSHRWALTAHCFETYSYDLSDPGGMVQFGLTSMPSFWSLQAYYTRYF 120

QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGYIK 193
Db 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWGYIK 180

QY 194 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAAGQKDACFGDSGG 253
Db 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAAGQKDACFGDSGG 240

QY 254 PLACNKNGLWYQIGVSWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 313
Db 241 PLACNKNGLWYQIGVSWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300

QY 314 FFPLLWALPLIGPV 327
Db 301 FFPLLWALPLIGPV 314
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RESULT 6
US-09-907-824-257
; Sequence 257, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257

LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-257
Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0
QY 14 MGARGALLALLARAGLRKPESQEAAPLSPGQRRRVITSRIVGGBDAELGRNPWQSLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGQRRRVITSRIVGGBDAELGRNPWQSLR 60
QY 74 LWDSHVGVSLLSHRWALTAHCFETYSDDLSPSGMNVQFGOLTSMPFSFSLQAYTRYF 133
Db 61 LWDSHVGVSLLSHRWALTAHCFETYSDDLSPSGMNVQFGOLTSMPFSFSLQAYTRYF 120
QY 134 VSNIVLSPRYLGNPSYDIALVKLSAPVTYTKHIQPICLQASTFFEFNRTDCWVTGWYIK 193
Db 121 VSNIVLSPRYLGNPSYDIALVKLSAPVTYTKHIQPICLQASTFFEFNRTDCWVTGWYIK 180
QY 194 EDEALPSPHTLOEVOVAIINNSMCNHLFLKYSFKDIFGDMVCAGNAGGKDACFGDSGG 253
Db 181 EDEALPSPHTLOEVOVAIINNSMCNHLFLKYSFKDIFGDMVCAGNAGGKDACFGDSGG 240
QY 254 PLACNKNGLWYQIGVSWGVGCGRPNRPVYVYTNISHHFEMIQKLMQAGSMGSDPPSWPLL 313
Db 241 PLACNKNGLWYQIGVSWGVGCGRPNRPVYVYTNISHHFEMIQKLMQAGSMGSDPPSWPLL 300
QY 314 FPPLLMALPLLPV 327
Db 301 FPPLLMALPLLPV 314

RESULT 7

US-09-907-841-257
; Sequence 257, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-841-257

Query Match 96.4%; Score 1728; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPMQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPMQGSRLR 60

QY 74 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDPSGMVQFGQLTSMPSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDPSGMVQFGQLTSMPSLQAYYTRYF 120

QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLOASTFFENRTDCWVTGWGIK 193
DB 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLOASTFFENRTDCWVTGWGIK 180

QY 194 EDEALPSHTQGEVOVAIINSMCNHLEFKYSFKDIPGDMVCAGNAGGKDACFGDSGG 253
DB 181 EDEALPSHTQGEVOVAIINSMCNHLEFKYSFKDIPGDMVCAGNAGGKDACFGDSGG 240

QY 254 PLACNKNGLWYQIGVVSVGCGRENRPVYTNISHHFEWIKLMAQSGMSQDPSPNELL 313
DB 241 PLACNKNGLWYQIGVVSVGCGRENRPVYTNISHHFEWIKLMAQSGMSQDPSPNELL 300

QY 314 FPPLLWALPLGPV 327
DB 301 FPPLLWALPLGPV 314

RESULT 8

US-09-904-011-257
; Sequence 257, Application US/09904011
; Publication NO. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPMQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRWPMQGSRLR 60

QY 74 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDPSGMVQFGQLTSMPSLQAYYTRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDPSGMVQFGQLTSMPSLQAYYTRYF 120

QY 134 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLOASTFFENRTDCWVTGWGIK 193
DB 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVTTYTKHIQICLOASTFFENRTDCWVTGWGIK 180

QY 194 EDEALPSHTLOEVQVAIINNSMCNHLFLKYSPRKDIIFGDMVVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSHTLOEVQVAIINNSMCNHLFLKYSPRKDIIFGDMVVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 313
DB 241 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 314 FPLLLWALPLIGPV 327
DB 301 FPLLLWALPLIGPV 314

RESULT 9
US-09-906-742-257
; Sequence 257, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-742-257
Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAEIGRWPWQSLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAEIGRWPWQSLR 60
QY 74 LWDHVGCVSLLSHRWALTAHCFETYSDLSDFSGMWVQFQLTSMPSFWSLQAYTRYF 133
DB 61 LWDHVGCVSLLSHRWALTAHCFETYSDLSDFSGMWVQFQLTSMPSFWSLQAYTRYF 120
QY 134 VSNITLSPRYLGNSPYDIALVLSAPVYTKHIQPICLQASTFEFENRTDCWVTGMYIK 193
DB 121 VSNITLSPRYLGNSPYDIALVLSAPVYTKHIQPICLQASTFEFENRTDCWVTGMYIK 180
QY 194 EDEALPSHTLOEVQVAIINNSMCNHLFLKYSPRKDIIFGDMVVCAGNAQGGKDACFGDSGG 253
DB 181 EDEALPSHTLOEVQVAIINNSMCNHLFLKYSPRKDIIFGDMVVCAGNAQGGKDACFGDSGG 240
QY 254 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 313
DB 241 PLACNKGMLWQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 314 FPLLLWALPLIGPV 327
DB 301 FPLLLWALPLIGPV 314
RESULT 10
US-09-906-838-257
; Sequence 257, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-906-838-257

Query Match
Best Local Similarity 96.4%; Score 1728; DB 10; Length 314;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLAKPESQBAAPLSGPGGRVITSRIVGGEDAEELGRWPGQSLR 73
DB 1 MGARGALLALLARAGLAKPESQBAAPLSGPGGRVITSRIVGGEDAEELGRWPGQSLR 60
QY 74 LWDHVCVGLSHRWALTAACFCFTYSDLPSCGMVQFGOLTSMPFSWLSQAYTYRF 133
DB 61 LWDHVCVGLSHRWALTAACFCFTYSDLPSCGMVQFGOLTSMPFSWLSQAYTYRF 120
QY 134 VSNVILSPRYLGNSPYDIALVKLSAPVVTYTKHQICLQASTFPEFNTDCWVTGWGIK 193
DB 121 VSNVILSPRYLGNSPYDIALVKLSAPVVTYTKHQICLQASTFPEFNTDCWVTGWGIK 180
QY 194 EDEALPSPTLQEVQVAINNSNCNHLFLKYSFRKDIQDMVCAGNAOGKDACFGDSGG 253
DB 181 EDEALPSPTLQEVQVAINNSNCNHLFLKYSFRKDIQDMVCAGNAOGKDACFGDSGG 240

; 254 PLACNKGGLWYQIGVWSGVCGRPNRPGVYTNISHHFHWIKLMAQSGMSQDPSPWPLL 313
; 241 PLACNKGGLWYQIGVWSGVCGRPNRPGVYTNISHHFHWIKLMAQSGMSQDPSPWPLL 300
; 314 FFPLLMALPLILGPV 327
; 301 FFPLLMALPLILGPV 314

RESULT 11
US-09-907-613-257
; Sequence 257, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
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; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-257

Query Match          96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGEDAEELGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGEDAEELGRWPQGSRLR 60

QY 74 LWDHSHVCGVSLLSHRWALTAHCFETYSYDLSDPGGMVQFQGLTSMPSFWSLQAYTRYF 133
DB 61 LWDHSHVCGVSLLSHRWALTAHCFETYSYDLSDPGGMVQFQGLTSMPSFWSLQAYTRYF 120

QY 134 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 193
DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 180

QY 194 EDEALPSHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFDGSGG 253
DB 181 EDEALPSHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFDGSGG 240

QY 254 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
DB 241 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300

QY 314 FFPLLWALPLLGVPV 327
DB 301 FFPLLWALPLLGVPV 314

RESULT 12
US-09-907-942-257
; Sequence 257, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,942
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-942-257

Query Match          96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGEDAEELGRWPQGSRLR 73
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGGRRVITSRIVGGEDAEELGRWPQGSRLR 60

QY 74 LWDHSHVCGVSLLSHRWALTAHCFETYSYDLSDPGGMVQFQGLTSMPSFWSLQAYTRYF 133
DB 61 LWDHSHVCGVSLLSHRWALTAHCFETYSYDLSDPGGMVQFQGLTSMPSFWSLQAYTRYF 120

QY 134 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 193
DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK 180

QY 194 EDEALPSHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFDGSGG 253
DB 181 EDEALPSHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFDGSGG 240

QY 254 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 313
DB 241 PLACNKNGLWYQIGVSWGCGRRNRPVYTNISHHFEWIKLMAQSGMSQDPDSWPLL 300

QY 314 FFPLLWALPLLGVPV 327
DB 301 FFPLLWALPLLGVPV 314
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RESULT 13
US-09-904-859-257
; Sequence 257, Application US/09904859
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,859
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257

; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-859-257
Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. NO. 1.8e-161; Indels 0; Gaps 0;
Matches 314; Conservative 0; Mismatches 0;
QY 14 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITRIVGGEAEALGRWPQGSRLR 73
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITRIVGGEAEALGRWPQGSRLR 60
QY 74 LWDSHVCGVSLSHRWALTAACFETYSDSLSDPSGMVQFCQLTSMSEFSLQAYTRYF 133
Db 61 LWDSHVCGVSLSHRWALTAACFETYSDSLSDPSGMVQFCQLTSMSEFSLQAYTRYF 120
QY 134 VSNLYLSPRYLGNSPYDIALVKLSAPVYTYTHIQICLQASTFFEFNRDCWVTGWYIK 193
Db 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTYTHIQICLQASTFFEFNRDCWVTGWYIK 180
QY 194 IDEALPSPHTLOEVQVVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAGGKACFGDSGG 253
Db 181 IDEALPSPHTLOEVQVVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAGGKACFGDSGG 240
QY 254 PLACNKGWLYQIGVWSMGVCGRPNRPGVVTNISHHFEWIKLMAQSGMSQPDPSWPLL 313
Db 241 PLACNKGWLYQIGVWSMGVCGRPNRPGVVTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 314 FPFLWALPLLPV 327
Db 301 FPFLWALPLLPV 314
RESULT 14
US-09-909-204-257
; Sequence 257, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,204
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-204-257

Query Match 96.4%; Score 1728; DB 10; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.8e-161;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 MGARGALLALLARAGLRKPSQEAAPLSGPGRRVITSRVGGEDAEALGRWPQGSILR 73
DB 1 MGARGALLALLARAGLRKPSQEAAPLSGPGRRVITSRVGGEDAEALGRWPQGSILR 60
QY 74 LWDSHVCGVSLLSHRWALTAACFCFETYSLDSPSGMWVQFGLTSMFSPWSLQAYTYRYF 133
DB 61 LWDSHVCGVSLLSHRWALTAACFCFETYSLDSPSGMWVQFGLTSMFSPWSLQAYTYRYF 120
QY 134 VSNYILSPRYLGNPSYDIALVKLSAPVYTKHIQPIQLOASTFEPENRTDCWVTGNGYIK 193
DB 121 VSNYILSPRYLGNPSYDIALVKLSAPVYTKHIQPIQLOASTFEPENRTDCWVTGNGYIK 180
QY 194 EDEALSPHTLOBQVVAIINNSMCHLFLKYSPKXDFGDMVCAGNAQGGKACFGDSGG 253
DB 181 EDEALSPHTLOBQVVAIINNSMCHLFLKYSPKXDFGDMVCAGNAQGGKACFGDSGG 240
QY 254 PLACNKNGLWYQIGVWSWGVGCGRRPNRPVYTNISHHFWIQLKMAQSGMSQFDPSPWLL 313
DB 241 PLACNKNGLWYQIGVWSWGVGCGRRPNRPVYTNISHHFWIQLKMAQSGMSQFDPSPWLL 300
QY 314 FFFLLWALPLLPV 327
DB 301 FFFLLWALPLLPV 314

RESULT 15
US-09-904-820-257
; Sequence 257, Application US/09904820
; Publication No. US20030036094A1
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; TITLE OF INVENTION: Acids Encoding the Same
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Best Local Similarity 100.0%; Pred. No. 1.8e-161;

Matches	314;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	14	MGARGALLALLARAGLRKPEAOEAPLSGPCGRRVITSRIVGGEDAEILGRWPMQGS LR	73						
Db	1	MGARGALLALLARAGLRKPEAOEAPLSGPCGRRVITSRIVGGEDAEILGRWPMQGS LR	60						
Qy	74	LWDSHVCVSVLLSHRWALTAHCFETYSDLSDFSGMWQFGQLTSMPSFWSLQAYYTRYF	133						
Db	61	LWDSHVCVSVLLSHRWALTAHCFETYSDLSDFSGMWQFGQLTSMPSFWSLQAYYTRYF	120						
Qy	134	VSNITLSPRVLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK	193						
Db	121	VSNITLSPRVLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGIK	180						
Qy	194	EDEALPSPHTLQEVQVAIIINSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSG	253						
Db	181	EDEALPSPHTLQEVQVAIIINSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSG	240						
Qy	254	PLACNKNGLWYQIGVWSWGVCGGPRNRPVYTNISHHFEWIQKLMQSGMSQDPSPWLL	313						
Db	241	PLACNKNGLWYQIGVWSWGVCGGPRNRPVYTNISHHFEWIQKLMQSGMSQDPSPWLL	300						
Qy	314	FFPLLWALPLIGPV	327						
Db	301	FFPLLWALPLIGPV	314						

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